```
Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                          Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
:
        110
110
                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq
        5525522552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
      100.0
100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    June 17, 2002, 12:36:25; Search time 94.14 Seconds (without alignments)
14.159 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-367-714A-23
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
\SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
\SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
\SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
                                                                                                                                                                                                          Length DB
        12
12
12
12
13
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapext 0.5
      19
19
21
21
21
21
21
21
21
21
                                                                                                                                                                                                            IJ
     AAW82850
AAW82856
AAB17413
AAB17416
AAB17483
AAB17485
AAW35231
AAB17482
                                                                                                                                      AAW35149
AAW35152
AAW82847
                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747574
Leu/Lys diastereom Leu/Lys diastereom Antipathogenic pep Diastereomer pepti Antipathogenic pep Antipathogenic pep Diastereomer pepti Antipathogenic pep
                                                                                                                                                                                                        Description
```

•	_	_			Ī	_	_	_		-		_			_	Ī							-		_								
40	40	40	40	40	41	41.5	43	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	52	52	52	52
76.9	4	2		76.9																												100.0	100.0
16	16	15	14	14	28	15	73	153	21	21	14	13	13	12	12	12	12	12	12	12	12	. 12	12	12	12	12	12	12	12	77	77	37	14
16	16	15	21	16	10	19	21	20	22	22	19	21	18	21	21	21	21	21	19	19	19	19	19	19	18	18	18	18	18	19	19	19	19
AAR67798	AAR67797	AAR56957	AAB17122	AAR67795	AAP91335	AAW77384	AAB52057	AAY29393	AAB60066	AAU03187	AAW82855	AAB17484	AAW35232	AAB17422	AAB17421	AAB17420	AAB17417	AAB17414	AAW82887	AAW82886	AAW82885	AAW82857	AAW82851	AAW82848	AAW35171	AAW35170	AAW35169	AAW35153	AAW35150	AAW82859	AAW82858	73	AAW82854
Monoamine derivati	Bisamine derivatiz	Peptide which neut	Calmodulin antagon	Antimicrobial olig		Lytic peptide with		Sperm whale myoglo	KL3 membrane activ	Ф	Antipathogenic pep	Antipathogenic pep	m											Antipathogenic pep					H		thogenio	Lytic peptide with	Antipathogenic pep

ALIGNMENTS

RESULT AAW35149

AAW35149;

AAW35149 standard; peptide;

12 Å

Leu/Lys diastereomer 14-APR-1998 (first entry)

peptide [D]-L3,4,8,10-K4L8.

```
Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                        Synthetic
20-FEB-1997;
                                                           Modified-site
                                                                                             Misc-difference
                                                                                                              Misc-difference
                                 WO9731019-A2
                                                                            Misc-difference
                                                                                                                                Misc-difference
                28-AUG-1997.
97WO-IL00066
                                                                                              /note=
8
                                                                                                                                Location/Qualifiers
                                                           /note-
12
                                                                            /note=
10
                                                                                                                       /note= "D-form residue"
                                                   /note=
                                                   "C-terminal amide"
                                                                    "D-form residue"
                                                                                    "D-form residue"
                                                                                                       "D-form residue"
```

```
RESULT AAW35152
ID AAW7
XX AAW7
XX AAW7
XX Leu
DE Leu
KW Honn
KW Honn
KW ACO
XX Synt
XX Synt
XX Key
FT Misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on CC invention. The peptides of the invention have: (a) cytolytic activity on CC the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The peptides, their complexes and mixtures are used to treat CC infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer; in human and veterinary medicine. Also, they can be used as agricultural pesticides. The absence of haemolytic activity (associated CC with disturbance of alpha-helical structures) means that the peptides thave few if any toxic effects, and those that include D-aa will have concreased resistance to proteolytic degradation. Nor haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, corresistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                      Synthetic
                      Misc-difference
                                                             Misc-difference
                                                                                                             Misc-difference
                                                                                                                                                          Misc-difference
                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW35152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 39; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Leu/Lys diastereomer peptide [D]-K1,5,9,12L2,6,7,11-K4L8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35152 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 kliikliiklik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96IL-0117223.
                         /note= "D-form residue"
                                                                                                                                                        /note= "D-form residue"
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                /note= "D-form 5
/note=
"D-form residue
                                                                                       "D-form residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52; DB 18; Length 12;
Pred. No. 0.053;
; Mismatches 0; Indels
                                                                                                                                 residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

₽ Qy

>

```
RESULT
AAW82847
ID AAW8
В
                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on the peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogens and malignant cells not naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The peptides, their complexes and mixtures are used to treat infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides have few if any toxic effects, and those that include D-aa will have chose that include T-activity allowing selection of agentastion. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
             Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21; Page 40; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
Misc-difference 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
Misc-difference 11
                                                                        Antipathogenic peptide.
                                                                                                         19-MAY-1999
                                                                                                                                          AAW82847
                                                                                                                                                                      AAW82847 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oren Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9731019-A2
                                                                                                                                                                                                                                                    1 kliikliiklik 12
                                                                                                                                                                                                                                                                                   1 KLLLKLLKLLK 12
                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue"
12 `
/note= "C-terminal amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "D-form residue"
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                  Score 52; DB 18;
Pred. No. 0.053;
                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      0;
```

0;

```
밁
 PD XXW XXX PD XXX
                                                                                                                                                                                                                                                                  ď
                                                                                                                                                                                                                                                                                AAW82850
                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a pathogenic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               solutions for wetting contact lenses, as preservatives, e.g., cosmetic and food industries, as pesticides (e.g. fungicides bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 105; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9837090-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
27-AUG-1998
                              WO9837090-A1
                                                               Synthetic
                                                                                              cancer; infection; disinfectant; contact lens we
preservative; pesticide; fungicide; bactericide.
                                                                                                              Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                              Antipathogenic peptide
                                                                                                                                                                                                19-MAY-1999
                                                                                                                                                                                                                                 AAW82850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                AAW82850 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide which has a net positive charge greater than 1, comprises L-amino
                                                                                                                                                                                                                                                                                                                                                   L
                                                                                                                                                                                                                                                                                                                                                                                  1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                   k111k111k11k 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as disinfectants for destruction of microorganisms, i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-IL00081
                                                                                                                                                                                                                                                              peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                100.
                                                                                                                                                                                                                                                                                                                                                                                                                                  .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .08;
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 19 Pred. No. 0.053; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
the
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

```
AAW82856
                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present peptide is used to produce the agents of the invention. The CC specification describes a non-haemolytic, cytolytic agent, which is a CC peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copolymer. The agent has a selective cytolytic activity on CC pathogenic cells. The agent has a selective cytolytic activity on CC peptide which has a net positive charge greater than 1, comprises L-amino CC acid residues and/or D-amino acid residues and comprises an alpha-helix CC breaker molety, or a peptide (or cyclic derivative of this) which CC (comprises L-amino acid residues and D-amino acid residues, has a net CC (comprises L-amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of concer or for treatment of several diseases caused by pathogens, CC including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in CC cosmetic and food industries, as preservatives, e.g., in the CC cosmetic and food industries, as pesticides (e.g. fungicides or cCC bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-594464/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
               20-FEB-1997;
                                              19-FEB-1998;
                                                                               27-AUG-1998
                                                                                                                W09837090-A1
                                                                                                                                             Synthetic
                                                                                                                                                                                preservative;
                                                                                                                                                                                                cancer;
                                                                                                                                                                                                              Non-haemolytic;
                                                                                                                                                                                                                                                Antipathogenic peptide.
                                                                                                                                                                                                                                                                               19-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                  AAW82856;
                                                                                                                                                                                                                                                                                                                                               AAW82856 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLLLKLLLKLLK 12
|||||||||||
| 1 klllklllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                    Çī
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity
12; Conser
                                                                                                                                                                                                infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-IL00081
               97WO-IL00066
                                                98WO-IL00081
                                                                                                                                                                                              cytolytic; selective cytolytic activity; pathogen;
on; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 19;
0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
```

0;

Oren

2,

cancer

```
The present peptide is used to produce the agents of the invention. The CC specification describes a non-haemolytic, cytolytic agent, which is a CC peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent has a selected from a cyclic derivative of a comprises L-amino acid residues and/or D-amino acid residues and comprises un alpha-helix cc peptide which has a net positive charge greater than 1, comprises L-amino acid residues and comprises an alpha-helix cc comprises L-amino acid residues and D-amino acid sequence such that c comprises L-amino acid residues an amino acid sequence such that c a corresponding amino acid sequence comprising only L-amino acid residues are consitive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, cincluding bacterial, fungal, viral, mycoplasm and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoinmune disease; cytostatic; autiashmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TMD; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte autigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                  23-OCT-1998;
22-OCT-1999,
                                                                                                                          25-OCT-1999;
                                                                                                                                                                                  04-MAY-2000
                                                                                                                                                                                                                                         WO200024782-A2.
                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antipathogenic peptide sequence SEQ ID NO:517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17413 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KILLKLLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 52; DB 19; 1 Similarity 100.0%; Pred. No. 0.053; 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA;
                                  980S-0105371
990S-0428082
                                                                                                                          99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising an CC (XI)a=I-(X2)b, where: If = an Fc domain; XI and X2 = are each (XI)a=I-(X2)b, where: If = an Fc domain; XI and X2 = are each (XI)a=I-(X2)b, where: If = an Fc domain; XI and X2 = are each (I)c-Pl - (I)c-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNP; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                              23-OCT-1998;
22-OCT-1999;
                                                                                                                                               25-OCT-1999;
                                                                                                                                                                                                          04-MAY-2000
                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antipathogenic peptide sequence SEQ ID NO:520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17416 standard; Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 39; Page 378; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an pharmacologically active peptides, useful autoimmune diseases -
      (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                  WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLLLKLLKLLK 12
|||||||||||||
1 klllklllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative 0
                                                              98US-0105371.
99US-0428082.
                                                                                                                                                  99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 21;
Pred. No. 0.053;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fc domain and for treating
```

0;

0; Gaps

0;

Length 12; Indels

g Q

δ

```
RESULT E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC fc domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (X1)a+F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1 -(L2)d-P2 -(L2)d-P2.

CC (L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of

CC pharmacologically active peptides; L1, L2, L3, and L4 = are each independently

CC independently linkers; and a, b, c, d, e, and f = are each independently

CC or 1, provided that at least 1 of a and b is 1. The composition can

CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

CC activities. DNAs, vectors and host cells from the present invention can

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC The use of an Fc domain (rather than a Fab domain) can provide a longer

CC half-life or incorporate functions such as Fc receptor binding, protein

CC h binding, complement fixation, and possibly placental transfer. AAA69443

CC concerned with the examplification of the present invention acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                           23 FOCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                      cytotoxic T cell lymphocyte antigen vascular endothelial growth factor;
                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cance autoimmune disease; Cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; anta MMPB; inhibitor; erythropoietin; thrombopoietin; interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige
                                                                                                                   04-MAY-2000
                                                                                                                                               WO200024782-A2
                                                                                                                                                                           Synthetic
                                                                                                                                                                                                         asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                        Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                      AAB17483;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17483 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacologically active
               (AMGE-) AMGEN
                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ட்.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          k111k111k11k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               composition of matter comprising an acologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Page 379; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                           98US-0105371
99US-0428082
                                                                                      99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J,
                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone
                                                                                                                                                                                                                                  thrombopoietin; interleukin 1; igen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                           ID NO:587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fc domain and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matter (I) comprising and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                 antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLYMPIA NO CONTRACTOR OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC (Xl)a-F1-(X2)b, where: F1 = an Fc domain; Xl and X2 = are each confidence independently selected from -(Ll)c-P1, -(Ll)d-P2-(L3)d-P2.

CC (Xl)a-F1-(X2)b, where: F1 = an Fc domain; Xl and X2 = are each confidence independently selected from -(Ll)c-P1, -(Ll)d-P2-(L3)d-P2.

CC (Ll)c-P1-(L2)d-P2-(L3)e-P^3, or -(Ll)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC (where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently confidence in the composition can provide a longer confidence in the composition can provide a longer confidence in the composition and confidence in the composition can confidence in the composition can confidence in the composition can provide a longer confidence in the composition can composition can confidence in the composition can composition can composition can composition can compositio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T cell lymphocyte antigen 4; tumour necrosis vascular endothelial growth factor; matrix metalloprote asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombol
immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF;
MMP; inhibitor; erythropoietin; thrombopoietin; interle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antipathogenic peptide sequence SEQ ID NO:589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U,
                                                                                                                             23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                  04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2
                                                                                                                                                                                                                                   25-OCT-1999;
                                                              (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||||||
1 klllklllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 401; 608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                             98US-0105371
99US-0428082
                                                                                                                                                                                                                                   99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     describes composition of matter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiasthmatic; thrombolytic; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (I) comprising (ers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is
```

0,

Feige U,

Liu C,

Cheetham J,

Boone

TC;

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (I) comprising an CC (XI)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (CC -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (CC where P1, P2, P3, and P4 = are each independently sequences of comparation of the peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently contained that at least 1 of a and b is 1. The composition can composition are contained for producing pharmaceutical compositions. The compositions are considered for producing pharmaceutical compositions. The compositions are consequenced for producing pharmaceutical compositions. The compositions are consequenced for producing pharmaceutical compositions of the use of an Fc domain (rather than a Fab domain) can provide a longer lalf-life or incorporate functions such as Fc receptor binding, protein a hinding, complement fixation, and possibly placental transfer. AAA69443 cc sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                               20-FEB-1997;
                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial ce agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer autoimmune diseases \boldsymbol{\cdot}
                                                                                                                         W09731019-A2
                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35231 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 kliikliiklik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 402; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide [D]-L3,4,8,10-K4L8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                           /note-
                               97WO-IL00066
                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; S
100.0%; F
tive 0;
                                                                                                                                                                    "D-form residue
                                                                                                                                                                                                                                                                "D-form
                                                                                                                                                                                                                      "D-form
                                                                                                                                                                                                                                                                                                                "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 21
Pred. No. 0.053;
; Mismatches
                                                                                                                                                                                                                   residue
                                                                                                                                                                                                                                                                   residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial cell lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
  AC XXX AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC sequence represents a diastereomer peptide of the invention. This CC sequence is used in a "bundle sequence", which is created by binding 5 CC copies of this sequence to peptide 23 (see ANM3514). The peptides of CC copies of this sequence to peptide 23 (see ANM3514). The peptides of CC and malignant cells not naturally present in the body; but (b) no CC haemolytic activity, or such activity only at a concentration CC significantly higher than that at which they lyse pathogens. The CC peptides, their complexes and mixtures are used to treat infections CC (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, CC in human and veterinary medicine. Also, they can be used as preservatives CC for food, cosmetics and agricultural produce, or as agricultural CC disturbance of alpha-helical structures) means that the peptides have few CC disturbance of alpha-helical structures) means that the peptides have few CC if any toxic effects, and those that include D-aa will have increased CC resistance to proteolytic degradation. Non-haemolytic, cytotoxic random CC copolymers of pardaxin, each has a specific spectrum of activity. Callowing selection of agents for particular applications. Since these CC random copolymers induce total lysis of bacterial cell walls, resistance CC for them is untilkely to develow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer autoimmune disease; cytostatic; antiasthmatic; thrombolytic; vi immunosuppressive; EPO; FPO; CTLA4; minetic; IL-1; TNF; antagon MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
23-OCT-1998;
                                                                                            04-MAY-2000
                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17482 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide(s) having selective cytolytic activity and mallgnant cells, but no haemolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-435088/40
                                             25-OCT-1999;
                                                                                                                                         WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Antipathogenic peptide sequence SEQ ID NO:586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  red. No. 0.057;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                against pathogens used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
```

0;

WPI; 1998-594464/50

```
RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXX PPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(Xl)a-Fl-(X2)b, where: Fl = an Fc domain; Xl and X2 = are each

independently selected from -(Ll)c-Pl, -(Ll)d-Pl-(L2)d-P2.

(Ll)c-Pl-(L2)d-P2-(L3)e-P^3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

where Pl, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; Ll, L2, L3, and L4 = are each independently

clindependently linkers; and a, b, c, d, e, and f = are each independently

clindependently linkers; and a, b, c, d, e, and f manunosuppressive

activities. DNAs, vectors and host crells from the present invention can

be used for producing pharmaceutical compositions. The compositions are

useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer

half-life or incorporate functions such as Fc receptor binding, protein

A binding, complement fixation, and possibly placental transfer. AAA6943

to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matt pharmacologically active autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 39; Page 401; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
             Oren Z,
                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                             Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                                                                                                                                                                                 AAW82854 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT+1999;
                                        (YEDA ) YEDA RES & DEV CO LTD
                                                                                                 19-FEB-1998;
                                                                                                                             27-AUG-1998
                                                                                                                                                          W09837090-A1
                                                                                                                                                                                                                 preservative;
                                                                                                                                                                                                                                                                          Antipathogenic
                                                                                                                                                                                                                                                                                                         19-MAY-1999
                                                                                                                                                                                                                                                                                                                                     AAW82854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                          \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLLIKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ç
                                                                                                                                                                                                               pesticide; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9905-0428082
                                                                     97WO-IL00066
                                                                                                                                                                                                                                                                         peptide
                                                                                                 98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matter comprising an tive peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 21; Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                  bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc domain and for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an
is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infection They may be used in both human and veterinary medicine. They may also used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid residues and/or D-amino acid residues and comprises an alpha-helix breaker modety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                             Biologically a
lipid bilayer
              acids which
                          New modified peptide(s) - obtained by substitution with an acid which is modifiable by a reaction and replacing other
                                                                                                                                                                      18-MAR-1997;
                                                                                                                                                                                                    18-MAR-1998;
                                                                                                                                                                                                                                                                WO9841535-A2
                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                            Lytic peptide
                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW77378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW77378 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present peptide is used to produce the agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 106; 126pp; English.
                                                                                                        Ajoula
                                                                                                                                      (ANMA-) ANMAT TECHNOLOGY LTD
                                                                                                                                                                                                                                 24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLKLLKLLK 12
                                                                                                        HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0
              are not to
                                                                                                        Clarke DJ
                                                                                                                                                                                                                                                                                                                           active peptide; hormone; drug; toxin;
r membrane; microorganism; parasite; v
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                            with alterable function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                      97GB-0005519
                                                                                                                                                                                                  98WO-GB00799
              be modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                              ω.
                                                                                                                                                                                                                                                                                                                              parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                           amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections. may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
```

0

Claim 7;

Page

33pp; English

8x3555555555555

The peptides AAW77376-W77390 can be modified by the method of the invention by substituting at least one amino acid of the peptide to provide a peptide having at least one amino acid which is modifiable by a reaction and replacing other amino acids in the peptide with amino acids which are not modifiable by the reaction. The methods can be used for the modification of biologically active peptides such as hormones, toxins and peptides which act on lipid bilayer membranes. The modified peptides can be used e.g. in the body of an animal or plant or parts in order to affect the structure or integrity or permeability of a foreign body such as a microorganism, parasite or virus present in the body of the animal or plant or within the cells of the body of the animal

Вþ Qy

11

22

1 KLLLKLLKLLK

Query Match Best Local Matches

Similarity

100.0%; 0;

Score 52; DB Pred. No. 0.1 0; Mismatches

0.16; DB 19; 0

Length 37; Indels

0,

0;

Conservative

Sequence

37

AA;

plant

```
RRESULT 1
AAAM8284
XX AAW8
XX AAW8
XX AAW8
XX AAW8
XX Non
XX Non
XX VOOR
XX VOOR
XX VOOR
XX 27-
XX 27-
XX 27-
XX VI
XX V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW82858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW82858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09837090-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a pathogenic cells. The agent is selected from a cyclic derivative of a cid residues and/or D-amino acid residues and comprises in alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which because L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                    present peptide is used to produce the agents of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-IL00081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA
```

including bacterial, fungal, viral, mycoplasma and proture. They may be used in both human and veterinary medicine.

```
888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AAW82859
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
            The present peptide is used to produce the agents of the invention. The CC specification describes a non-haemolytic, cytolytic agent, which is a CC peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copolymer. The agent has a selective cytolytic activity on CC peptide which has a net positive charge greater than 1, comprises L-amino CC peptide which has a net positive charge greater than 1, comprises L-amino CC peptide which has a net positive charge greater than 1, comprises In-alpha-helix CC acid residues and/or p-amino acid residues and comprises an alpha-helix (comprises I-amino acid residues and D-amino acid residues, has a net CC positive charge greater than 1 and has an amino acid sequence such that CC positive charge greater than 1 and has an amino acid sequence such that CC is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, concluding bacterial, fungal, viral, mycoplasma and protozoan infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. Including be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW82859 standard; peptide; 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW82859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipathogenic
                                                                                                                                                                                                                                                                                                         New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9837090-A1
                                                                                                                                                                                                                                                                          Claim 17; Page 107; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLLKLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

THIS PAGE BLANK (USPTO)

```
Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                            ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on
and is
                                                                                                                                                                                                                                                                                                               score
                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq
                                                                                                                                                                                                                                                                                                                                                                                                                           seq
                                                                                                                                                                                                                                                                                                    No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                         76.9
71.2
71.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-367-714A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                June 17, 2002, 12:38:45; Search time 46.42 Seconds (without alignments)
24.840 Million cell updates/sec
69.2
                                                                                                                                                                                                                                                                                                                                                                        PIR_71:*
                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283138 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KILLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
                                                                                                                                                                                                                                                                                                                                              pir1:*
pir2:*
pir3:*
                                                          984
986
1712
84
91
109
                                                                                                                                                                                       1896
                                                                                                                                                                                                2513
137
238
255
465
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
(c) 1993 - 2000 Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96089334 residues
                                 DJNVCP
T41809
C71618
                                                                   A69735
F71132
E95105
E97973
                                                                                                    в97109
G71932
                                                                                                                                                                                      S03747
                 G70155
                                                                                                                                              T03171
                                                                                                                                                                                                                                                            IJ
                                                                                                                                                               A70102
                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd
                                                                hypothetical prote
phage PBSX termina
probable nitrite r
ABC transporter, p
hypothetical prote
                                                                                                                                                                    small membrane pro
hypothetical prote
hypothetical prote
probable integral
                                                                                                                                                    conserved hypothet hypothetical prote
                                                                                                                                                                                                                                                          Description
        Phosphocarrier pro
RNaseP C5 chain -
                                         DNA-directed DNA p
                                                          colicin V secretio
                                                                                                           DNA-dependent RNA
                                                                                                                    hypothetical prote
hypothetical prote
probable transcrip
                                                                                                                                             hypothetical prote
probable antibioti
                                                                                                                                                                                                                 merozoite antigen
                                                                                                                                                                                                                          probable ABC
                                                                                                                                                                                                                                 uncharacterized pr
                        hypothetical
                                 hypothetical
                                                                                                                                                                                                         hypothetical prote
                                                                                                                                                                                                                                           hypothetical
                       prote
                                                                                                                                                                                                                                         prote
                                prote
                                                                                                                                                                                                                          trans
```

ALIGNMENTS

hypothetical protein F2J10.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96536
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G96536
A.;Accession: G96536 uncharacterized protein, Yje/RRF2 family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: A96914 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, F.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteriol. 183, 4823-4838, 2001 A;Reference number: A96900; MUID:21359325; PMID:21359325 RESULT G96536 RESULT A96914 A; Title: Genome Sequence and A; Reference number: A96900; A; Accession: A96914 A;Cross-references: GB:AE005173; NID:g8569097; PIDN:AAF76442.1; GSPDB:GN00141C;Genetics: A;Status: preliminary A;Molecule type: DNA A;Residues: 1-2513 <STO> A; Status: preliminary 멍 A; Map position: 1 A; Molecule type: DNA A; Residues: 1-137 <KUR> A;Gene: F2J10.9 Query Match Best Local Matches 797 LLLGLLLKLLK 807 Local Similarity tes 10; Conserv 2 LLLKLLLKLLK 12 N Conservative 76.9%; Score 40; DB Pred. No. 1.1e 0; Mismatches 1.1e+02; DB 2; Length 2513; Indels Solvent-Producing Bacterium 9 Gaps 0;

A;Cross-references: GB:AE001437; PIDN:AAK78100.1; PID:g15022941; GSPDB:GN00168

```
C.Accession: E71375
R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
Science 281, 375-388, 1998
A.Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Superfamily: unassigned ATP-binding cassette proteins; C:Keywords: ATP C:Keywords: ATP F:27-207/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A71250; MUID:98332770
A;Accession: E71375
A;Affarra.
B
                                      Qy
                                                                                                                                                                                                                                                                                                                                                    R;KO, C.; Smith II, C.K.; McDonell, M.
Mol. Biochem. Parasitol. 41, 53-64, 1990
A;Title: Identification and characterization of a target antigen A;Reference number: A06637; MUID:90348718
A;Recession: A60637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    merozoite antigen LPMC-61 - Elmeria tenella (fragment)
C;Species: Elmeria tenella
C;Dete: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-238 <COL>
A;Cross-references: GB:AE001188; GB:AE000520; NID:g33222
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable ABC transporter, ATP-binding protein - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-2000 C;Date: E71375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: C; Genetics: A; Gene: CAC0115
                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-255 <KOA>
A;Cross-references: GB:M30933
C;Keywords: tandem repeat
F;18-240/Region: glutamine-ric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 8
                                                                                                    Matches
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 RFLLKLLRKLIK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
  2 RLLLKLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLLLKLLLKLLK 12
                                            1 KLLLKLLKLL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LLKILLKILK 12
                                                                                              Similarity 81.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conser
                                                                                                                                                                                                                           glutamine-rich repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.2%;
80.0%;
                                                                                                                         71.2%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB Pred. No. 41; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ν,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                              Score 37; DB
Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB
Pred. No. 25;
2; Mismatches
                                                                                                                         DB 2;
44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID: g3322282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                              Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the syphilis spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAC65030.1; PID: 933222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                            of a monoclonal antibo
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cassette homology
                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 . ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gw1r
                                                                                                                                                                                                               A;Cross.references: EMBL:Y00526; NID:940181; PIDN:CAN68584.1; PID:940183
A;Cross.references: EMBL:Y00526; NID:940181, A.M., Alloni, G., Azevedo, V.; Beron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadais, Y.; Sato, T.; Scanl
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtill
A; Reference number: A69580; MUID:98044033
A; Astarise, numleis a614 segmenore not shown translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                    A; Gene: eag
C; Superfamily: Bacillus subtilis small membrane protein
                                                                                              A; Cross-references: GB: 299111;
A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 1
A; Introns: 47/1; 117/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T30155
                                                                       C; Genetics:
                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-143 <KUN>
                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-143 < PER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP: C37A2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 LLKIILKILK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LLKLLLKLLK 12
```

GB:AL009126;

NID:g2633699; PIDN:CAB13238.1;

PID:g26337

```
R;Perego, M.; Hoch, J.A.
Mol. Microbiol. 1, 125-132, 1987
A;Tille: Isolation and sequence of the spoOE gene: its role in initiation of A;Reference number: $03746; MUID:88260878
A;Accession: $03747
                                                                                                                       C;Species: Bacillus subtilis
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C;Accession: S03747; C69619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-465 < LEEP
A;Cross-references: EMBL:U97194; pIDN:AAB52449.1; GSPDB:GN00019; CESP:C37A2.5
A;Experimental source: strain Bristol N2; clone C37A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Le, T.T.; Kemp, K.; Scheet, P. submitted to the EMBL Data Library, April 1997 A;Description: The sequence of C. elegans cosmid C37A2. A;Reference number: Z20746 A;Accession: T30155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C37A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                     small membrane protein eag - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185/1; 264/3; 364/2; 426/2
                                                                                                                                                                                                                                                                                                                                                                                                                                           71.28;
                                                                                                                                                                                                                                                                                                                                                                                                                       ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
77;
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 465
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                       sporulat
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

```
R:Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kvrtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.V submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F1707
A:Reference number: Z14334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F1707.14 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #:C;Accession: T01490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                C;Geneti
A;Gene:
                                                                                                                                                                                                                                                                                                                                 R;Perna, N.T.; Pluḥkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; liller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamos Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number; A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Z3270 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1896 < YYS>
A; Cross-references: EMBL: ACO03671; NID: g2833627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
A; Introns: 11/3; 43/3;
                                                                                                                                                                                                                                                                                                A;Reference number: A85480;
A;Accession: G85837
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G85837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T01490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                  밁
                                                                              Qy
                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: G85837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 7
RESULT
                                                                                                                                                                                                                                 A; Experimental
                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                               A; Residues: 1-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                  Matches
                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LLEKMLLRFIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LLLKLLLKLLK 12
                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATSP:F1707.14
                                                                                 N
                                                                                                                                                                                                  Z3270
 9
                                                                               LLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLELMLKTLK 1842
                                                  MLLKLIKIFK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                                                                                Similarity 6; Conser
                                                                                                                                                                                                                                   source:
                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                  <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                 GB:AE005174; NID:g12516312; PIDN:AAG57163.1; ce: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112/3; 1803/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%;
72.7%;
                                                                                                                                  67.3%;
54.5%;
                                                                                                                Score 35; DB Pred. No. 17; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g3176689; GSPDB:GN00059; ATSP:F170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu, G.; Kwan, A.; Oji, O.;
Davis, R.W.; Ecker, J.R.; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1896
                                                                                                                                                 Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                   Glasner, J.D.; Rose, anta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                 GSPDB:GN00145; UWGP:Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Federspiel,
                                                                                                                                                                                                                                                                                                                                                                                   D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                   Apodaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s:
                                                                                                                                                                                                                                                                                                                                                                                                   Mayhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŀi
```

```
probable integral membrane protein Cj0421c [imported] - Campylobacter jejuni C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000 C;Accession: C81386 B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical integral membrane protein BB0017 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C;Accession: A70102 R;Fraser, C.M.; Casjens, B.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586; 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: serotype C; Genetics: A; Gene: Cj0421c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.W.; Quail, M.; Rajandream,
Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001116; GB:AE000783; NID:g2687896; A;Experimental source: strain B31 C;Superfamily: conserved hypothetical protein yitT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: A70102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74257.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-318 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: C81386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912
R;Dietrich, F.S. submitted to the EMBL Data Library, August 1995 A;Description: The sequence of S. cerevisiae co. A;Reference number: S69554
                                                                                                                  hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change
                                                                                                                                                                                        RESULT
S69625
                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-319 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 KLILKQIAKILK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLKLLK 12
                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                              1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                 S69625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ungall, K.; Ketley, J.M.; Churcher, C.; M.A.; Rutherford, K.M.; VanVliet, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                          DB _,
1.2e+02;
2;
                               cosmids 9410,
                                                                                                                       #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 318
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi
                             8035, 8166, and 9787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:AAC66414.1; PID:g268
                                                                                                                            23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                 0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.; Chil
nd, S.; Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (strain
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. Vu
```

A; Molecule type: DNA A; Residues: 1-3268 <DIE>

A; Accession:

S69625

рь Qy

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-53 <BAH>
A;Cross-references: EMBL:AF003534; NID:g2738385; PII
C;Superfamily: sillucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable antiblotic polypeptide - Chilo iridescent virus
(;Species: Chilo liridescent virus
(;Species: Chilo liridescent virus
(;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Aug-1999
(;Accession: T03171
(;Accession: T03171
R;Bahr, U. Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
Virus Genes 15, 235-245, 1997
Virus Genes 15, 235-245, MID: 11descent virus between the genome coordinates 0.101
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834, MID:98141693
A;Accession: T03171
A;Crafties. Tryellminary. translated from GR/FMRI/TDDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: EMBL:U33050; NID:g927726; PIDN:AAB64910.1; PID:g927738; MIPS:YDR457w
C.Genetics:
A.Gene: SGD:TOM1
A,Cross-references: SGD:S0002865; MIPS:YDR457w
A,Map position: 4R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
T03171
                                                                                                                                 Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                             Cross-references: GB:AE006641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94469.1; PID:g2738442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 LLKLVLKLL 523
                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 70. nes 7; Conservative
                                                                                                                                 Local Similarity es 8; Conser
                                                                                     4 LKLLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LLLKLLKLL 11
:|||:| |||
3 ILLKILFKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LLKLLLKLL 11
                                                                                                                                                                                                                                                    SS02227
                                           LKALLKLLK 43
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%;
88.9%;
                                                                                                                                                    65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%;
                                                                                                                                 Score 34; DB
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB
Pred. No. 33;
2; Mismatches
                                                                                                                                   0;
                                                                                                                                                                                                                                                                                          NID:g13815527; PIDN:AAK42397.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2; Le
Pred. No. 9.9e+02;
1; Mismatches 0;
                                                                                                             e 34; DB 2; Leny...
J. No. 1.1e+02;
-----hes 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٠.
                                                                                                                                                                             Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U07420; NID:g705344; PIDN:AAC43309.1; PID:g460971
R;Sauer, U.; Treuner, A.; Buchholz, M.; Duerre, P.
submitted to the EMBL Data Library, June 1993
A;Description: Sigma factor homologous genes in C. acetobutylicum.
A;Reference number: S34306
A;Accession: S34309
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 46-146, Pp.148-235 <SAU>
A;Cross-references: EMBL:Z23079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable transcription initiation factor sigma E - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999 C;Accession: I40627; S34309 C;Accession: I40627; S34309 C;Accession: I40627; S34309 C;Accession: I40627; Sass, C; Bennett, G.N. Gene 153, 89-92, 1995 A;Title: Sequence and arrangement of genes encoding sigma factors in Clostridi A;Accession: I40626; MUID:95189110 A;Accession: I40626; MUID:95189110 A;Status: preliminary; translated from GB/EMBL/DDBJ A;MOJecule type: DNA A;Residues: 1-235 CRES-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T24H24.20 ~ Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress) c; Species: Arabidopsis thaliana (mouse-ear cress) c; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999 c; Date: 17-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999 c; Accession: T01464

R; Courtney, L.; Stoneking, T.; Langston, Y.; Mead, K. submitted to the EMBL Data Library, August 1998 A; Description: The sequence of A. thaliana T24H24.

A; Reference number: Z14333
A; Accession: T01464
A; Reference number: Z14333
A; Accession: T01464
A; Reference number: Z14333
A; Accession: T01464
                                                                                          ф
                                                                                                                        QY
                                                                                                                                                                                                                                                                                             C;Superfamily: transcription initiation factor signa K; transcription initiation fact C;Reywords: DNA binding; sigma factor; transcription initiation factors: F;60-235/Domain: transcription initiation factor sigma katF homology <KTF>
                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 4
A; Introns: 48/1; 102/3
A; Note: T24H24.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-213 <COUY
A;Cross-references: EMBL:AF075598; NID:g3293581; PID:g3377838
A;Experimental source: cultivar Columbia
                                                                                                                                                 Query Match
Best Local Similarity /2...
**Conservative**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.4
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorrange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 QLILKLLLPLSK 211
completed: June 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLKLLLKLLK 12
                                                                                          2
                                                                                                                   1 KLLLKLLLKLL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.48;
                                                                                                                                                                                                   65.48;
  2002, 12:42:57
                                                                                                                                                                                  Score 34; DB 2;
Pred. No. 1.3e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 2; Le
Pred. No. 1.2e+02;
Pred. No. 2; Mismatches 2;
                                                                                                                                                                                                                           Length 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factors in Clostridium acet
                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                     Gaps
```

0;

В Q

B Qy

Ó

Job time: 252 sec

THIS PAGE BLANK (USPTO)

V

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein protein search, using sw model

Run on: June 17, 2002, 12:39:45 ; Search time 21.35 Seconds (without alignments) 21.763 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-367-714A-23 52 1 KLLLKLLLKLLK 12

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
	Score
67. 2 67. 2 67. 2 67. 3 67. 3 67. 4 67. 3 67. 4 67. 3 67. 4 67. 3 67. 4 67. 3 67. 3 67. 4 67. 3 67. 4 67. 3 67. 3	1
1943 1943 1943 433 986 986 31 109 333 334 334 334 334 334 483 334 487 209 201 201 201 204 204 204 204 204 204 204 204 204 204	20 i D
	DB
	ID
5714 eimeria te 6630 bacillus ge hc10 homo sapis 3657 clostridis 9786 bacillus ge 8131 autographa 1712 bombyx mor 3039 mycoplasma 3039 mycoplasma 3039 mycoplasma 3039 mycoplasma 1708 rattus nor 7708 rattus nor 7708 rattus nor 1708 mus muscul 1154 mus muscul 1154 mus muscul 2185 mus sprett 8918 mor sapis 8918 homo sapis 8019 phoca vittus 2185 homo sapis 819 phoca vittus 6563 bos taurus 1705 homo sapis 1705 homo sapis 1706 homo sapis 1707 rattus nor 1718 mus scrofilus se 1707 rattus nor 1718 mus scrofilus se 1718 mus scrofilus scrofilus se 1718 mus scrofilus scr	Description

Query Match 71.2%; Best Local Similarity 80.0%; Matches 8; Conservative

; Score 37; DB: ; Pred. No. 15; 2; Mismatches

1; Length 238; Indels

0;

Gaps

0;

45	44	43	42	41	40	39	38	37	36	35	34
31	<u>3</u> 1	31	31	31	ω	3 1	32	32	32	32	32
59.6	59.6	59.6	59.6	59.6	59.6	59.6	61.5	61.5	61.5	61.5	61.5
231	231	231	229	193	193	159	3744	2470	2124	1941	1472
ш	۲	Н	ب	<u> </u>	_	۲	Ь	_	سا	ب	1
SOML_SCIOC	SOM2_SPAAU	SOM1_SPAAU	SOML_TETMU	INF3_CHICK	INF1_CHICK	YIB6_YEAST	YHP9_YEAST	TOR1_YEAST	Y192_HUMAN	UBR1_KLULA	A2MG_RAT
Q9ygk7 sciaenops o		sparus	Q9i9h4 tetraodon n				P38811 saccharomyc			o60014 kluyveromyc	w

ALIGNMENTS

Ωy

ω

```
В
                                                                                                                                       Qγ
                                                                                                                                                                                   Matches
                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                        \mathtt{REPEAT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it was by non-profit institutions as long as its content is in no was a superior of the content of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M30933; AAA29079.1; -. PIR; A60637; A60637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90348718; PubMed-2200963;
KO C., Smith C.K. II, McDonell M.;
"Identification and characterization of a target antige monoclonal antibody directed against Eimeria tenella me Mol. Biochem. Parasitol. 41:53-64(1990).

-I-FUNCTION: UNKNOWN. THE GLN-RICH TANDEM REPEATS MAY FOR AN UNKNOWN. ASPECT OF THE PARASITIC LIFE CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L_EIMTE
LP61_EIMTE
P15714;
01-APR-1990
01-APR-1990
                                                                                             N
                                                                                                                                       ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria.
NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence up
01-FEB-1994 (Rel. 28, Last annotation
Antigen LPMC-61 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Sporozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                              KLLLKLLLKLL 11
                                                                                   RLLLKLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MAY BE COVALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO FORM THE 80 kDa ANTIGEN,
DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE SPORULATION OF THE OOCYSTS AND IN THE SPOROZOITES FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LLKLLLKLLK 12
|:||:||||
3 LVKLVLKLLK 62
                                                                                                                                                                                 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sporozoite; Repeat;
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                255 AA;
                                                                                                                                                                                                                                                                                                                                                                  18
49
58
66
79
91
104
141
153
165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60637
                                                                                                                                                                                                                                                                                   48
57
65
78
90
103
140
152
164
172
192
210
255
31267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
                                                                                                                                                                                             71.2%;
81.8%;
                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                 12 X APPROXIMATE TANDEM REPEATS, GLN-
RICH.

1.
2.
3.
4.
5.
6.
7.
10.
11.
                                                                                                                                                           Score 37; DB 1;
Pred. No. 16;
1; Mismatches
                                                                                                                                                                       1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sporulation.
                                                                                                                                                                                                                                                                          8C5E6005FFFC2DB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a target antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                             1,
                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tenella merozoites.";
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE IMPORTANT
MAY BE AN
                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        b
                                                                                                                                                   Gaps
                                                                                                                                                 0;
OTOF_HUMAN
ID OTOF_H
AC OPHCIO
DT Ol-MAR
DT Ol-MAR
DT Ol-MAR
DT Ol-MAR
DT Ol-MAR
OTOFO
OS HOMO S
OC EUKARY
OC MAMMAL
OX NCBI
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
RG JSSUE
RX MEDLIN
RO TISSUE
RX MEDLIN
RO TISSUE
RX MEDLIN
RO TISSUE
RX MEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD RESERVED TO COLOR COLOR COLOR RESERVED TO COLOR COLOR COLOR RESERVED TO COLOR COLOR RESERVED TO COLOR COLOR COLOR RESERVED TO COLOR CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
```

```
Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                  Yasunaga S., Grati M., Chardenoux S., Lalwani A.K., Wilcox E.R., Petit C., 'OTOF encodes multiple long and short the long ones underlie recessive deafn Am. J. Hum. Genet. 67:591-600(2000).
MEDLINE=99206603; PubMed=10192385;
                                            TISSUE=Feta]
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             TISSUE=Brain; MEDLINE=20395831; PubMed=10903124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTOF_HUMAN STANDARD; PRT; 1997 AA. Q9HC10; Q9HC09; Q9Y650; Q9HC08; Q1-MAR-2002 (Rel. 41, Created) Q1-MAR-2002 (Rel. 41, Last sequence update) Q1-MAR-2002 (Rel. 41, Last annotation update) Otoferiln (Fer-1 like protein 2).
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y00526; CAA68584.1; --
EMBL; 299111; CAB13238.1; --
PIR; S03747. S03747.
SubtiList; BG10770; eag.
Hypothetical protein; Sporulation; Complete proteome.
Hypothetical protein; MW; D7410B50963D7A75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 LLLKMLLRFIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to licenseelsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restriction by the produced through the surpression of the surpres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-88320878; pubMed=2838724; Perego M., Hoch J.A.; "Isolation and sequence of the spoOE gene: its spoulation in Bacillus subtilis."; Mol. Microbiol. 1:125-132(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAG_BACSU
P06630;
01-JAN-1988
01-JAN-1988
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Be Bacillus/Staphylococcus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
(Rel.
1 16.4
                                                        (ISOFORM 4).
                                                                                                                                                                                                                                                                                                (ISOFORMS 1; 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06,
06,
40,
kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update;
Last annotation update;
protein in SPOOE 3'region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus/Clostridium group;
us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                  deafness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                            isoforms:
ness DFNB9.
                                                                                                                                                                                                                                                                                             3),
                                                                                                                                                                                                    Smith T.N., Friedman T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no rest
                                                                                                                                                                                                                                                                                                AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                  genetic evidence that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration
Loutstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no
on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

```
SOFT TITTET TO THE TEST TO THE TEST TO BE READED BE READED BE READED BE READED BE READED.
               ρ
 ₽
                                      Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yasunaga S.,
Salem N., El-
"A mutation i
                                                                                        CONFLICT
                                                                                                                                                                      VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
EMBL;
 1965
                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                              PROSITE; PS00499; C2_DOMAIN_1; PROSITE; PS50004; C2_DOMAIN_2; Transmembrane; Repeat; Alternat
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFNB9, a no
Nat. Genet.
                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 21:363-369(1999).
                                                                                                                                          VARSPLIC
                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                       DOMA'IN
                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                    MIM;,601071;
                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sunaga S., Grati M., Cohen-Salmon M., El-Amraoui A., lem N., El-Zir E., Loiselet J., Petit C.; mutation in O'DF, encoding otoferlin, a FER-1-like pNB9, a nonsyndromic form of deafness.";
                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recessive deafness 9 (DFNB9).
SIMILARITY: BELONGS TO THE FERLIN
SIMILARITY: CONTAINS 4 C2 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Isoform 1 and isoform 3 are brain. Isoform 2 is expressed in the fetus and heart, placenta, skeletal muscle and kidney. DISEASE: Defects in OTOF are the cause of nonsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type II membrane protein (By ALTERNATIVE PRODUCTS: at least 4 isoforms; 1/long 2/short-1, 3/short-2 and 4/short-3; are produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vesicle-plasma membrane fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                  AF183185;
AF183186;
AF183187;
AF107403;
 LLLKLLLLLL
                   LLLKLLLKLL
                                                                                                                                                                                                                                                                                                                                                                PF00168; C2;
                                                                                                                                                                                                                                                                                                                                                                                                       P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                               SM00239;
                                       Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                            IPR000008;
                                                                                                                                                                                                            1964
1985
241
404
947
1479
1303
1314
1965
                                                                                        1088
1997
                                                                                                                                          1943
                                                                                                                                                                                          1245
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 AAG12991.1; -.; AAG12992.1; -.; AAG17468.1; -.; AAD26117.1; -.
                                                                                                                                                                                                                                                                                                                                              C2; 6.
1974
                    11
                                                                                        1088
AA; 226735
                                                                                                                                                                                                                                                                                                                                                       C2DOMAIN.
                                                                                                                                                                      1984
1997
338
514
1052
1577
1310
1320
1983
747
1264
690
                                                                                                                                          1997
                                                                                                                                                                                                                                                                                                                                                                            C2.
                                                67.3%;
90.0%;
                                                                                                                                                                                                                                                                                                            OMAIN_1; 2.
OMAIN_2; 4.
Alternative splicing;
                                                                                                                            POTENTIAL.

EXTRACELLULAR (POTENTIAL).

C2 DOMAIN 1.

C2 DOMAIN 2.

C2 DOMAIN 3.

C2 DOMAIN 4.

POLY-LYS.
                                      Score 35; DB
Pred. No. 2.4e
0; Mismatches
                                      0,
                                                                                        ΜW;
                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                    IIKIVLALLGLLMLGLFLYSLPGYMVKKLLGA
                                                                                                           ISOFORM
                                                                                                  'n
                                                                                       L (IN REF. 1; AAG12991)
39D10CB5220638AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY.
                                               DB 1; 1
2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                              Deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonsyndromic autosoma:
                                                         Length 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e found
in adul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
(shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mustapha M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain,
                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its
                                      0;
```

```
RPSE_CLOADA
AC PASSAC
AC PASSAC
AC PASSAC
AC PASSAC
AC PASSAC
AC PASSAC
DT 01-FEB
DT 16-CCT
DT 16-CCT
DT 16-CCT
COS CLOSTIC
OC CLOSTIC
OC NCBL]
RN [1]
RN [1]
RN [1]
RN [1]
RN [2]
RN [2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIKAIN=ATCC 824 / DSM 792 / VKM B-1787;
Santangelo J.D., Kuhn A., Treuner A., Durre P.;
"Sporulation and time course expression of sigma genes in Clostridium acetobutylicum ".
Suhmiterod occurrence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994
01-OCT-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sauer U., Treuner A., Buchholz M., Santangelo J.D., Durre "Sporulation and primary sigma factor homologous genes in acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
Noelling J. Breton G. Omelchenko M.V., Maka
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti
Tatusov R.L., Sabathe F., Doucette-Stamm L.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 176:6572-6582(1994).

-I- FUNCTION: THE SIGNA FACTOR IS AN INITIATION FACTOR THAT PROMOT ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES THEN IS RELEASED. THIS SIGNA FACTOR IS RESPONSIBLE FOR THE EXPRESSION OF SPORULATION SPECIFIC GENES (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE SIGNA-70 FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-
STRAIN-ATCC 824 / DSM 792 / VKM B-
MEDLINE-95189110; PubMed-7883192;
Wong J., Sass C., Bennett G.N.;
"Sequence and arrangement of genes
Clostridium acetobutylicum ATCC 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 46-235 FROM N.A. STRAIN-ATCC 824 / DSM 792 / MEDLINE-95050216; PubMed-796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA polymerase sigma-E
SIGE OR CAC1695.
                                                                                                                                                                                                                      EMBL; U07420; AAC43309.1; -. EMBL; Z23079; CAA80617.1; -. EMBL; AE007679; AAK79661.1;
                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium acetobuty Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPSE_CLOAB
                                                                                                                                                                   PIR; $34309; $34309.
HSSP; P00579; 1SIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes in Clostridium acetobutylicum.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153:89-92(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30, Last seq. 40, Last ann. gma-E factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes encoding 
rcc 824.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nko M.V., Makarova K.S., Zenç
Qiu D., Hitti J., Wolf Y.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-1787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AN INITIATION FACTOR THAT PROMOTES AND SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sigma factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soucaille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daly M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
```

factor; DNA-directed

RNA

polymerase;

```
RESULT STANGLE STANGLE
Д
                                                           Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 8
                                                                                                                                                                    Query Match
Best Local
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9436463; PubMed-8083174;
MCDOnnell G.E., Wood H., Devine K.M., McConnell D.J.;
McDonnell D.J.;
McD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DNA_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z70177; CAA94059.1; -. EMBL; Z34287; CAA84048.1; -. EMBL; Z99110; CAB13115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
Krogh S., O'Reilly M., P
Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                                                                                          PIR; $47115; $47115.
SubtiList; BG11000; xtmB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-76 FROM N.A. STRAIN=168 / SOll3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.

Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P39786;
01-FEB-1995 (Rel. 31, Created)
01-CT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
PBSX phage terminase large subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XTMB_BACSU
38
                                                               4 LKLLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLKLLLKLL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
LKIVLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFLLRLLSKLL
                                                                                                                              Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
202
147
235 AA;
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
46
                                                                                                                                                                                                                                                                                           Complete proteome.

AA; 51150 MW; 471FC77DFEA2CA10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 I
221 I
147 I
26969 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%;
                                                                                                                                                                    65
77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nolan
o the E
                                                                                                                                                                . 48;
                                                                                                                              Score 34; DB
Pred. No. 85;
2; Mismatches
                                                                                                                                  Ÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n N., Devine K.M.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYMERASE CORE BINDING (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY).
L -> P (IN REF. 4).
; C726E18E6C93A903 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲.
                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                              Length 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              0,
```

```
DPOL_NEVAC

DPOL_N

AC PH8131

DT 01-NOV

DT 15-DEC

DE DNA POOL

OS AUTOGE

ON NCBL_T

RP SEQUEN

RR POLLY

RR POLLY

CC -1- S.

CR POLY

RR PINT

DR PINT

DR PINT

DR PINT

DR PANT

DR 
  DPOL_NPVBM
ID DPOL_N
AC P41712
DT 01-NOV
DT 15-DEC
DT 15-DEC
                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                RESULT
                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                          Matches
DPOL_NPVBM S
P41712; O92430;
01-NOV-1995 (Rel
15-DEC-1998 (Rel
15-DEC-1998 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P18131;
01-NOV-1990
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; DNA-directed DNA polymera
DNA-binding; Early protein
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., I
"The complete DNA sequence of Autographa californica
polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOY-1990 (Rel. 16, Created)
01-NOY-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF03104; DNA_pol_B_exo; 1.
PRINTS; PR00106; DNAPOLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M20744; AAA46692.1; -. EMBL; L22858; AAA66695.1; -. PIR; A31832; DJNVCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE~89073763; PubMed~3059678; Tomalski M.D., Wu J.G., Miller L.K.; "The location, sequence, transcription, baculovirus DNA polymerase gene."; Virology 167:591-600(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPOL_NPVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleopolyhedrovirus.
NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Autographa californica nuclear
Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + {DNA}(N).
-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002064; DNA_pol_B.
                                                                                                                                                                                                                          566 IVVKLLLKLL 575
                                                                                                                                                                                                                                                                         2 LLLKLLLKLL 11
                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724
946
830
(Rel. 32, Created)
(Rel. 37, Last sequence up)
(Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             960
830
114307
                                                                                                                                                                                                                                                                                                                                             65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ASP.

R -> W (IN REF. 1).

MW; 156ABB6BA1B45A21
                                                                                                                                                                                                                                                                                                                       Score 34; DB 1;
Pred. No. 1.8e+0
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAT-ATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyhedrosis virus (ACMNPV).
stage; Baculoviridae;
                                                                                                  986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          984 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and regulation
                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                   .8e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                      Length 984;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ⊸see R.D.;
a nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       0;
```

polymerase

(EC

2.7.7.7)

```
RESULT 9
                                                                                                                                                                                                 GN DT DT AC
                                                                                                           В
                                                                                                                            ρ
                                                                                                                                               Query Match
Best Local S
Matches 7
                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                               LPL_BUCRP
Q53017;
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO02064; DNA_pol_B. Pfam; PF00136; DNA_pol_B; 1. Pfam; PF03104; DNA_pol_B_exo; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombyx mori nuclear polyhedrosis virus (BmNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                 01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of nucleopolyhedrovirus.";
Submitted (OCT-1998) to the EMBL/Ger-1- CATALYTIC ACTIVITY: N deoxynucle
                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00106; DNAPOLB. SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D16231; BAA03756.1; -. EMBL; L33180; AAC63738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gomi S., Majima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaeychomsri S., Ikeda M., Kobayashi M., 
"Nucleotide sequence and transcriptional polymerase gene of Bombyx mori nuclear po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95133178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Leu operon l
LEUL OR LEUO
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                            DNA-binding;
                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virology
                                                                                                           566 IVVKLLLKLL 575
                                                                                                                            Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + {DNA}(N).
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY
                                                                               ဖ
                                                                                                                            LLLKLLLKLL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                PS00116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206:435-447(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long
          leader
                                                                                                                                                                                                 986
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                           Early
                                                                                                                                                                                                                                                                                                                       DNA-directed DNA
                                                                                                                                                                                                 AA;
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                               DNA_POLYMERASE_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7831799;
                  35,
35,
                                                                                                                                                                                                          , protein.
727
951
959
116
245
245
250
258
479
941
                                                                                                                                                                                                 114418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maeda S.;
                                                                                                                                                         65.48;
70.08;
                  Last sequence update)
Last annotation update)
                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N deoxynucleoside triphosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 ₩,
                                                                                                                                                                                                                                             POLY-LYS.
POLY-ASP.
POLY-ASP.
A -> S (I
H -> Y (I
                                                                                                                                                 <u>ω</u>
                                                                                                                                                                                                          TA -> AG
S -> G (I
N -> NDN
                                                                                                                                                          Score 34;
Pred. No.
                                                                                                                                                                                                                                       V # # A
                                                           PRT;
                                                                                                                                                                                                                                                                                                                     polymerase; DNA replication;
                                                                                                                                                Mismatches
                                                                                                                                                                                                 503E39F4A0BCC125 CRC64;
                                                                                                                                                                                                                                       NI)
NI)
NI)
NI)
NI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bombyx mori
                                                                                                                                                                                                                   (IN REF. 1).
                                                                                                                                              1.8e+02;
0;
                                                          31
                                                                                                                                                                                                            (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al analysis of the DNA polyhedrosis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no
                                                                                                                                                                                                                                       REF.
REF.
                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                    F. 1).
7. 1).
F. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   its content
                                                                                                                                                                  Length 986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diphosphate
                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    no
                                                                                                                                                                                                                                                                                                                                                                                                                                                    way
                                                                                                                                                                                                                                                                                                                                                                                                                                                              its
                                                                                                                                                0;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPA_MYCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                             C STRAIN-ATCC 27343;

X MEDLINE-94051609; PubMed-8233831;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

A Miyata M., Sano K.-I., Okada R., Fukumura T.;

T "Mapping of replication initiation site in Mycoplasma capricolum

T genome by two-dimensional gel-electrophoretic analysis.";

T Nucleic Acids Res. 21:4816-4823(1993).

C -!- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence

from pre-tRNA to produce the mature 5'terminus. It can also

c cleave other RNA substrates such as 4.55 RNA. The protein

C cleave other RNA substrates such as 4.55 RNA. The protein

C component plays an auxiliary but essential role in vivo by bindi

c to the 5'-leader sequence and broadening the substrate specifici

C of the ribozyme (By similarity).

C -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPA_MYCCA
P43039;
01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             padi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95333198; PubMed-7608990; MEDLINE-95333198; PubMed-7608990; Bracho A.M., Martinez-Torres D., Moya A., Latorre A.; "Discovery and molecular characterization of a plasmid localized Buchnera sp. bacterial endosymbiont of the aphid Rhopalosiphum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leader peptide; SEQUENCE 31 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ED
                                                                                                                                                                                                                                                                                                                                                 Mycoplasma
Bacteria; F
                                                                                                                                                                                                                                                                                                                                                                                                         Ribonuclease P protein component (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X71612; CAA50613.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=98793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera aphidicola (subsp. Rhopalosiphum padi).
Plasmid pRPE.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2095
                                                                                                                                                                                                                                                                                                                                   Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                               RNPA.
                                                                                                                                                                                                                                                                                                                                                                                             (RNase P protein) (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                          L6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLLLKLLLKLL
                                       protein subunit (By similarity) SIMILARITY: BELONGS TO THE RNPA
                                                                    extra-nucleotide from tRNA precursor. SUBUNIT: Consists of a catalytic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF LEUCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLLLLLLYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evol.
                                                                                                                                                                                                                                                                                                                                                  Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                capricolum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41:67-73(1995). THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leucine
A; 3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
81
                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthesis; Plasmid MW; 4D3E5E1C31C85413
                                                                                                                                                                                                                                                                                                                                                                                               C5).
                                          THE RNPA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                            n update)
: 3.1.26.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                    component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            (RNaseP protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
                                                                                                                                                                                     5'-leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                      Œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
                                                                      οŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL
                                                                                                 removing
                                                                      rnpB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                              specificity
                                                                                                                                          by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                   ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

This SWISS-PROT entry is copyright. between the Swiss Institute of Bio

Bioinformatics

It is

produced through

and

the

EMBL

a collaboration - MBL outstation

outstation

```
$-adenosylmethionine decarboxylase.";
Genomics 16:342-349(1993).
-i- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SamDC) [Contains: 5-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
                                                                                                                                                                                    141
SEQUENCE FROM N.A.
STRAIN=WISTAR; TISSUE=Spleen;
MEDLINE=93300506; PubMed=8314573;
MEDLINE=93300506; PubMed=8314573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1)
SEQUENCE FROM N.A.
MEDLINE-90215298; PubMed-2323572;
MEDLINE-90215298; PubMed-2323572;
MEDLINE-90215298; PubMed-2323572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-92038024; PubMed=1936275; MEDLINE-92038024; PubMed=1936275; Paulkka A., Ihalainen R., Aatsinki J., Paulkka A., Ihalainen R., Aatsinki J., Paulkka A., Ihalainen R., Paulkka A., Ihalainen R., Paulka A., Pau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of rat S-adenosylmethionine Comparison with an intronless rat pseudogene."; cene 86:193-199(1990).
                                                                                                                                     Pajunen A.;
"Structures and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89034205; PubMed=2460457;
ReJunen A., Crozat A., Jaenne O.A., Ihalainen R., Laitinen P.H.,
Stanley B., Madhubala R., Pegg A.E.;
"Structure and regulation of mammalian S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000100; Ribonuclease_P.
Pfam; PF00825; Ribonuclease_P: 1.
PROSITE; PS00648; RIBONUCLEASE_P: 1.
Hydrolase; Nuclease; Endonuclease; tRNA processing; RNA-binding.
SEQUENCE 109 AA; 12900 MW; ACF520A0982CDD12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D14982; BAA03619.1; -. HSSP; P25814; 1A6F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID~10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSKLLIKLIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLKLLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263:17040-17049(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
                                                                                                                                     localizations of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB Pred. No. 34; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                  A., Riviere M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmikangas P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pajunen
                                                                                                                                                                                                                                                                                                                                                                                                                    encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Α.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                  Szpirer
                                                                                                                                                                                                                                                                                                                                                                                                                    rat
                                                                                                                                     rat genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               decarboxylase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi; ; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                    ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ihalainen R.,
                                                                                                                                                                                                  ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
              DCAM_BOVIN

ID DCAM_B

AC P50243

AC P50243

DT 01-0CT

DT 16-CT

DT 16-CT

DE S-aden

DE (SamDt

DE (SamDt

OC Eukary

OC Mammal

OC Mammal

OC Moundad

OX NCBL_T

RN [1]

RP SEQUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $\frac{1}{2} \frac{1}{2} \frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M34464; AAA40683.1; EMBL; M64274; AAA42105.1; EMBL; 215109; CAA78814.1; J EMBL; Z15122; CAA78814.1; J EMBL; Z15123; CAA78814.1; J EMBL; Z15123; CAA78814.1; J PIR; J00439; DCRTDM.
PIR; S10487; S18487.
                                           Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammalia; Eutharia; C
Movidae; Bovinae; Bos
NCBI_TaxID-9913;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                 DCAM_BOVIN STANDARD; PRT; 334 AA.
P50243;
P50243;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50)
(SamDC) [Contains: S-adenosylmethionine decarboxylase alpha adenosylmethionine decarboxylase beta chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).

-i- SIMILARITY: BELONGS TO THE EUKARYOTIC ADONETDC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P17707; 1JEN.
InterPro; IPR001985; SAM_decarbox.
Pfam; PF01536; SAM_decarbox; 1.
ProDom; PD002379; SAM_decarbox; 1.
PROSITE; PS01336; ADOMETDC; 1.
              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 LLLKALVPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: PYRUVOYL GROUP,
PATHMAY: DECARBOXYLAFION OF S-ADENOSYLMETHIONINE PROVIDES THE
AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
BIOSYNTHESIS FROM PUTRESCINE.
SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
STRAIL COLUMN.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 72. 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biosynthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
146
38137 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                        Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333
                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 8 8
8 9 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyase; Decarboxylase; Pyruvate; Zymogen.
S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
CHAIN.
S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIERVAGE (MONHYDROLYTIC)
CONVERTED TO A PYRUVOTL GI
IMPORTANT FOR CAPALYTIC ASSIMILARITY).
IMPORTANT FOR CAPALYTIC ASSIMILARITY FOR CAPALYTIC ASSIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB Pred. No. 98; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H -> P (IN REF. 2).
A -> G (IN REF. 1).
; 9323E2D38BD8FEF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           μ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROUP.
ACTIVITY
```

ACTIVITY ACTIVITY

(BY (BY

(BY

0;

0

(AdoMetDC) a chain; S-

g QY

97

ω

11

DCAM_RAT P17708; 01-AUG-1990 01-JUL-1993 16-OCT-2001

Matches

RESULT 1
DCAM_RAT
DCAM_RAT
DCAM_RAT
AC P177
DT 01--DT 01--DT 01--DT 16--DT 1

decarboxylase.

Biol.

```
RESULT 13
DCAM_HUMAN
ID DCAM_H
AC P17707
DT 01-AUG
DT 01-AUG
DT 16-OCT
DE S-aden
DE (SamD)
DE (SamD)
OS Homo S
OS Homo S
OC Eukary
                                                                                                                                                                                                                                   Q
                                                                                                                                                    뫄
                                                                                                                                                                                     Query Match
Best Local S
Matches 8
_HUMAN DCAM_HUMAN STANK...
DCAM_HUMAN STANK...
P17707; Q9BWK4;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
(SamDC) "---thionine decarboxylase beta chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hill J.R., Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01536; SAM_decarbox; 1.
ProDom; PD002379; SAM_decarbox; 1.
PROSITE; PS01336; ADOMETDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mach M., White M.W., Neubauer M., De "Isolation of a cDNA clone encoding decarboxylase. Expression of the ge
                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86304300;
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                         Spermidine
                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocytes.";
J. Biol. Chem.
                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                        send
                                                                                                                                                                   2 LLLKLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETEC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS FROM PUTRESCINE SUBUNIT: HETEROTETRAMER OF TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: S-adenosyl-L-methionine = adenosyl)(3-aminopropyl) methylsulfonium salt COFACTOR: PYRUVOYL GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                    LLLKALVPLLK
                                                                                                                                                                                                                                                                                                                                                                                           M95605; AAA30359.1; -.
M14289; AAA30360.1; -.
P17707; JJEN.
Pro; IPR001985; SAM_decarbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long as its content d and this statement is not removed. Usage by an s requires a license agreement (See http://www.isb-an email to license@isb-sib.ch).
                                                                                                                                                                                     h 63.5%;
Similarity 72.7%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ဝှု
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XXX-1992) to
                                                                                                                                                                                                                                                                                                                                                        biosynthesis;
                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209-232 FROM
                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                        67
68
                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                   AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261:11697-11703(1986).
                                                                                                                                                    96
                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 FROM N.A.
PubMed=3017942;
                                                                                                                                                                                                                                                                                                                             334
                                                                                                                                                                                                                                                                                        8
8
8
8
                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                   38364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                               Lyase; Decarboxylase; Pyruvate; Zymogen. S-ADENOSYLMETHIONINE DECARBOXYLASE !
                                                                                                                                                                                                                                   ₩,
                                                                                                                                                                                    Score 33; DB Pred. No. 98; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                  IMPORTANT FOR (
SIMILARITY).
IMPORTANT FOR (
                                                                                                                                                                                                                                                                                     CHAIN.
CLEAVAGE (NONHYDROLYTIC)
CONVERTED TO A PYRUVOYL
IMPORTANT FOR CATALYTIC
                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                             S-ADENOSYLMETHIONINE
                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                   D8AFB98C9DD8A1E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Degen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                en J.L., Morris D.R.;
-adenosylmethionine
in mitogen-activated
                                                                                                                                                                                                                                                                                                           (NONHYDROLYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                               noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no
                                                                                                                                                                                                       Ļ
                                                                                                                                                                                                                                                   CATALYTIC
                                                                                                                                                                                                                                                                     CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                                     2
                                                                                                                                                                                                       Length 334;
                                                                                                                                                                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * (5-deoxy: + CO(2).
                                                                                                                                                                                                                                                                                                                             DECARBOXYLASE ALPHA
                                                                                                                                                                                                                                                                                                                                               DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                       GROUP.
ACTIVITY
                                                                                                                                                                                                                                                                     ACTIVITY
                                                                                                                                                                                                                                                    ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                      (BY
                                                                                                                                                                                                                                                    (BY
                                                                                                                                                                                                                                                                                       (BY
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o
                                                                                                                                                                                      0
```

```
MOD_RES
ACT_SITE
ACT_SITE
                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92011599; PubMed-1917972;
Stanley B.A., Pegg A.E.;
"Amino acid residues necessary for putrescine stimulation of human s
                                                                                                                                                       SITE
                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure 7:583-595(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ekstrom J.L., Mathews I.I., Stanley B.A., Pegg A.E., "The crystal structure of human S-adenosylmethionine 2.25-A resolution reveals a novel fold.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Choriocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decarboxylase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanley B., Madhubala R., "Structure and regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., MEDLINE-89034205; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
NCBI_TaxID=9606;
   MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinfi
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99306040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pajunen
                                                                                                                                                                                                                                                                                                                        Pfam; PF01536; SAM_decarbox;
                                                                                                                                                                                                                                                                                                                                                           MIM; 180980
                                                                                                                                                                                                                                                                                                                                                                                                PIR; A31786;
                                                                                                                                                                                                                                              3D-structure.
                                                                                                                                                                                                                                                                  Spermidine biosynthesis;
                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOSYNTHESIS FROM PUTRESCINE.
SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND
SIMILARITY: BELONGS TO THE EUKARYOTIC ADC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: S-adenosyl-L-methionine = adenosyl)(3-aminopropyl) methylsulfonium salt COFACTOR: PYRUVOYL GROUP.
ENZYME REGULATION: BOTH PROENZYME PROCESSING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY ARE STIMULATED BY PUTRESCINE;
PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES
AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
                                                                                                                                                                                                                                                                                                                                                                            1JEN; 01-JUN-99.
                                                                                                                                                                                                                                                                                                                                                                                                             M21154; AAA51716.1; -. BC000171; AAH00171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   M21154; AAA51716.1;
                                                                                                                                                                                                                                                                    PD002379; SAM_decarbox; 1.; PS01336; ADOMETDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial srequires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem. 263:17040-17049(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOV-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crozat
                                                                                                                                                                                                                                                                                                                                                                                                DCHUDM
                                          8
8
                                                                                                                  67
88
                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266:18502-18506(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10378277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2460457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A., Jaenne O.A.,
                                                                                                                                                                                        334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                             67
                                      82
                                                                                             68
68
11
                                                                                                                                                                                                                                                                                                                                        SAM_decarbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                Lyase; Decarboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pegg A.E.;
of mammalian
CLEAVAGE (NONHYDROLYTIC).

CONVERTED TO A PYROVOYL GROUP.

IMPORTANT FOR CATALYTIC ACTIVITY.

IMPORTANT FOR CATALYTIC ACTIVITY, AND
PUTRESCINE STIMULAION OF PROCESSING.

IMPORTANT FOR CATALYTIC ACTIVITY.

E-Q: LOSS OF ACTIVITY. NORMALL

PUTRESCINE-STIMULATED PROCESSING.

E-Q: LOSS OF ACTIVITY. LOSS OF
                                                                                                                                                                      S-ADENOSYLMETHIONINE CHAIN.
                                                                                                                                                                                                                             S-ADENOSYLMETHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ihalainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADOMETDC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.,
                                                                                                                                                                                                                                                                Pyruvate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laitinen P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (5-deoxy-5-
+ CO(2).
                                                                                                                                                                                          DECARBOXYLASE ALPHA
                                                                                                                                                                                                                             DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ealick S.E.;
decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE
                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at
```

```
RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local s
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1130:221-223(1992).

-I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
-I- COEACTOR: PYRUYOYL GROUP.
-I- PATHWAY: DECARBOXYLATION OF S-ADENOSYIMETHIONIUM PROVITED PROVIDED TO STANDARD PROVIDED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
5-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha adenosylmethionine decarboxylase beta chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MedLINE=92223099; PubMed=1562599;
Tekwani B.L., Stanley B.A., Pegg A.E.;
Tekwani B.L. stanley B.A., Pegg A.E.;
"Nucleotide sequence of hamster S-adenosylmethionine decarboxylase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Rodentia; Sciurogn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P28918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCAM_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LILKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETIC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE BIOSYNTHESIS FROM PUTRESCINE.
SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                           X63861; CAA45343.1;
S19871; DCHYDM.
S22358; S22358.
; P17707; LJEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLKALVPLLK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 72.
8; Conservative
    IPR001985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
247
249
146
334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
49
61
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
247
249
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49
61
67
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38325
SAM_decarbox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTRESCINE-STIMULATED PROCESSING.
E-Q: LITTLE EFFECT.
C-A: LITTLE EFFECT.
E-Q: LITTLE EFFECT.
E-Q: LITTLE EFFECT.
K-A: GREATLY REDUCED CATALYTIC ACTULTY. NO PUTRESCINE-STIMULATED PROCESSING.
C-A: LOSS OF ACTIVITY. GREATLY REDUCE PUTRESCINE-STIMULATED PROCESSING.
C-A: LITTLE EFFECT.
E-Q: LITTLE EFFECT.
E-Q: LITTLE EFFECT.
E-Q: ACTIVILE EFFECT.
E-Q: LITTLE EFFECT.
E-Q: ACTIVILE EFFECT.
E-Q: LITTLE EFFECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB Pred. No. 98; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> A (IN REF. 2).
F78F93AAE28A92DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GREATLY REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AdoMetDC)
a chain; S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
DCM1_MC
ALD DEPTH REPORT OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SO STATE TO SERVICE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
```

δã

日

1

```
Pfam; PF01536; SAM
ProDom; PD002379; PROSITE; PS01336; A
Spermidine biosynth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILT 15

__DMOUSE __DMUISE __DMI_MOUSE __STANDARD; PRT; 334 AA.

P31154;
01-7UL-1993 (Rel. 26, Created)
01-7UL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-adenosylmethionine decarboxylase proenzyme 1 (EC 4.1.1.50)
1 (SamdC 1) [Contains: S-adenosylmethionine decarboxylase 1
chain; S-adenosylmethionine decarboxylase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
MOD_RES
ACT_SITE
                                                                                                                  STRAIN-129/SVJ; TISSUE-Spleen; STRAIN-129/SVJ; PubMed-10570962; MEDLINE-20035739; PubMed-10570962; Nishimura K., Kashiwagi K., Matsuda Y., Jaenn "Gene structure and chromosomal localization s-adenosylmethionine decarboxylase.";
S-adenosylmethionine decarboxylase.";

Gene 238:343-350(1999)
-1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
-1- COPACTOR: DECAROXYLATION OF S-ADENOSYLMETHIONINE PROVIDES
-1- PATHWAY: DECAROXYLATION OF S-ADENOSYLMETHIONINE PROVIDES
-MINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE
                                                                                                                                                                                                                                                                  MEDILINE-93345510; PubMed-8344293;
Suzuki T., Sadakata Y., Kashiwagi K., Hoshino K., Kakinuma Y., Shirahata A., Igarashi K.;
"Overproduction of S-adenosylmethionine decarboxylase in ethylglyoxal-bis(guanylhydrazone)-resistant mouse FM3A cells.";
Eur. J. Biochem. 215:247-253(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waris T., Ihalainen R., Keraenen M.-R., Pajunen A.; "Molecular cloning of the mouse S-adenosylmethionine decarboxylase CDNA: specific protein binding to the conserved region of the mRNA 5/-untranslated region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=93345510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=93080592; PubMed=1449993;
Waris T., Ihalainen R., Keraenen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 189:424-429(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 LILKALVPLIK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biosynthesis;
1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAM_decarbox; 1.
79; SAM_decarbox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADOMETEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
8
8
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyase; Decarboxylase; Pyruvate; Zymogen.
S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN.

CLEAVAGE (NONHYDROLYTIC).

CONVERTED TO A PYRUVOYL GROUP.

IMPORTANT FOR CATALYTIC ACTIVITY

SIMILARITY).

IMPORTANT FOR CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN.
S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
IMPORTANT FOR CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FB519BCA749A1A7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                           Jaenne O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                0.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 334;
                                                                                                                                                mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY
                                                                                                                                                                Igarashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AdoMetDC alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus
                       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

Ç

```
Search completed: June 17, 2002, 12:44:45 Job time: 300 sec
                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z14986; CAA78710.1; -.
EMBL; D12780; BAA02243.1; -.
EMBL; B025024; BAA83784.1; -.
HSSP; P17707; IJEN.
MGD; MGI: 88004; Amdl:
InterPro; IPR001985; SAM_decarbox.
Pfam; PF01536; SAM_decarbox; 1.
                                                                                                                                                                                                                                                                                                                                                                            SITE
MOD_RES
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSYNTHESIS FROM PUTRESCINE.
-!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS SIMILARITY).
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETDC FAMILY.
                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002379; SAM_decarbox; 1. PROSITE; PS01336; ADOMETEC; 1.
                                                                                                86 LLLKALVPLLK 96
                                                                                                                    2 LLLKLLLKLLK 12
|||| || || ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis;
                                                                                                                                                                                                                                                                   334 AA;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                68
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
                                                                                                                                                                                                                                                                 38272 MW;
                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                        63.5%;
72.7%;
                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyase; Decarboxylase; Pyruvate; Zymogen.
S-ADENOSYLMETHIONINE DECARBOXYLASE 1 BETA
                                                                                                                                                                      <u>بــ</u>
                                                                                                                                                                                        Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                      ALPHA CHAIN.
CLEAVAGE (NONHYDROLYTIC).
CONVERTED TO A PYRUVOYL GROUP.
IMPORTANT FOR CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                 SIMILARITY).
; 7950A1E9A9ACBD72 CRC64;
                                                                                                                                                                                                                                                                                          SIMILARITY).
IMPORTANT FOR CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
IMPORTANT FOR CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN.
S-ADENOSYLMETHIONINE DECARBOXYLASE 1
                                                                                                                                                                      red. No. 98;
Mismatches
                                                                                                                                                                      2:
                                                                                                                                                                                                           Length 334;
                                                                                                                                                                      Indels
                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
                                                                                                                                                                      Gaps
                                                                                                                                                                      0;
```

Вþ Qy

THIS PAGE BLANK (USPTO)

4.5

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                     NO.
  score
and is
                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
BG
                                                                                                                                                     Score
                                                                                                                                                                                               is
                                                                                                                                                                                                                                                                                                                                                                                                                                       seq
  4-4 NO O O O O O O O O O O O O O
                                                                                                                                                                                                        greater
                                                                                                                                                                                               derived
                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                length:
                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                   is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
 76.9
76.9
71.2
69.2
69.2
69.2
69.2
69.2
67.3
67.3
                                                                                                                                                                                                                                                                                                                                                                                                  Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 17, 2002, 12:39:25 ; Search time 73.61 Seconds (without alignments) 28.202 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-367-714A-23
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                      sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
                                                                                                                                                                                                                                                                                                                sp_organelle:*
                                                                                                                                                                                                                                                                                                                      sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                 sp_human:*
                                                                                                                                                                                                                                                                                                                                                         sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                  sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                sp_mammal:*
                                                                                                                                                                                                                                         sp_bacteriap:*
                                                                                                                                                                                                                                                 sp_rvirus:*
                                                                                                                                                                                                                                                                           sp_virus:*
                                                                                                                                                                                                                                                                                     sp_rodent:*
                                                                                                                                                                                                                                  sp_archeap:*
                                                                                                                                                                                                                                                           sp_unclassified: *
                                                                                                                                                                                                                                                                  sp_vertebrate:*
                                                                                                                                                                                                                                                                                             sp_plant:*
                                                                                                                                                                                                                                                                                                                                          p_invertebrate:*
                                                                                                                                                     Length
 237
1107
1453
1896
263
318
319
1230
1307
1307
1997
                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapext 0.5
                                    16
16
                                                                                                 10
                                                                                                                  16
                                                             Q9G9H3
O64604
                                                                                                       Q97MS6
Q9BC70
Q9HC09
Q9HC10
Q03280
                                                                                       Q94LQ5
Q96LK7
                          Q9Y650
                                                                                                                                                    Ħ
                                    Q9CP24
Q9PI84
O51049
                                                                               Q95XU2
                                                                                                                          Q9FR53
Q9LPM4
                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562222
       Q961k7 homo sapien
Q95x2 caenorhabdi
Q95x3 cshizophyll
Q999h3 schizophyll
Q964604 arabidopsis
Q9cp24 pasteurella
Q9p184 campylchact
Q51049 borrelia bu
Q9y650 homo sapien
Q9h601 homo sapien
                                                                                      Q9fr53 arabidopsis
Q91pm4 arabidopsis
Q97m86 clostridium
Q9bc70 sargassum p
Q941q5 oryza sativ
Q961k7 homo sapien
 003280
                                                                                                                                                   Description
homo sapien
homo sapien
homo sapien
saccharomyc
```

63.5	63.5	63.5	63.5	63.5	63.5	33 63.5 100	63.5	63.5	63.5	63.5	63.5	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4
					_	16 Q932M8	_	16 051404						5 Q9NDI1		0			ဂ္ဂ								0557	5 Q9GR26
staphyloco	Q9yfw9 aeropyrum p	Q97s99 streptococc	Q950q3 spizellomyc	Q9g905 ochromonas		Q932m8 staphylococ				Q99yw0 streptococc	Q91fk0 chilo iride	Q9nef9 drosophila	O96160 plasmodium	Q9ndil drosophila	Q9nkd6 drosophila	Q9vz85 drosophila	Q9pe08 xylella fas	Q97rbl streptococc	O58557 pyrococcus	Q973p4 sulfolobus	ī	z1z4	ש	Q9ac69 staphylococ	7wi9 sulfol	1fx6	758 chilo	r26 a

ALIGNMENTS

```
Ş
               Query Match
Best Local Similarity
Watches 10; Conserve
                                                                                             Q9FR53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                            Pfam; PF02259; FAT; 1.

Pfam; PF02250; FAT; 1.

Pfam; PF00454; PI3_PI4_kinase; 1.

SMART; SM00146; PI3KC; 1.

SMART; SM00146; PI3KC; 1.

PROSITE; PS00915; PI3_4_KINASE_1; 1.

PROSITE; PS50290; PI3_4_KINASE_3; 1.

SEQUENCE 2481 AA; 279187 MW; DA663
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Menand B., Nussaume L., Meyer C., Desnos T., Bouchez D.,
"Mutation in AtTOR affects embryo development.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIN9867; AAG43423.1; -.
HSSP; P42345; IFAP.
                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                               TOR.
                                                                                                                                                                                        InterPro; IPR003151;
InterPro; IPR003152;
InterPro; IPR000403;
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                           PTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FR53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FR53
 2 LLLKLLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                        ; FATC.
; PI3_PI4_kinase.
                                         76.9%;
                            0,
                                       Score 40; DB 10;
Pred. No. 1.7e+02;
                            Mismatches
                                                                                               DA663EA9A9366F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                    Length 2481;
                             Indels
                                                                                                                                                                                                                                                                                        Robaglia C.;
                            0;
                            Gaps
                            0;
```

Вр

785

LLLGLLLKLLK

795

```
RESULT
OPTMS6
AC
OPTMS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPARATION OF STREET OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LPM4;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakano H., Liu S.X., Yu G., Lee J., Lenz C., Pham P., Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B. Miranda M., Nguyen M., Palm C., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; Theologis A.; Theologis A.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AC015445; AAF76442.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00146; PI3KC; 1.

PROSITE; PS00915; PI3_4_KINASE_1;
PROSITE; PS00916; PI3_4_KINASE_3;
PROSITE; PS50290; PI3_4_KINASE_3;
SEQUENCE 2513 AA; 282911 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
   Gibson R
Tatusov
                             SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
Noelling J., Breton G., Omelchenko M.V.,
Gibson R., Lee H.M., Dubois J., Qiu D., F
                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum. Bacteria; Firmicutes; Bacillus/Clostridium Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                        Q97MS6;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
UNCHARACTERIZED PROTEIN, YJE/RRF2 FAMILY.
CAC0115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC015445; AAF
HSSP; P42345; 1FAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F2J10.9 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9LPM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F2J10.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q97MS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                   NCBI_TaxID=1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LLLKLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLGLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00454; PI3; SM00146; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003151; FAT.
IPR003152; FATC
IPR000403; PI3_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
       Sabathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PI4_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PI3_PI4_kinase
       F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
15,
19,
       Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB Pred. No. 1.7e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲
                                        Qiu D., Hitti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A4B9740321AC5261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
L.7e+02;
       Makarova K.S.,
Hitti J., Wolf!
L., Soucaille!
                                                                                                                                                                                                                                                                                                                          group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2513;
                                            , Zeng
Y.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  im C., Lam B.,
Davis R.W.,
           Daly M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosidae;
                                                                                 0.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

1

pb Qy

25

LLLKLLLKLLK
:|||| ||:||
ILLKLQLKVLK

ဌဌ

N

```
RESULT
Q9BC70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA RT RT RT RT DR DR DR DR DR COR SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                           Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
          Query Match
Best Local
 Matches
                                                  Carbon dioxide fixation; Chloroplast; Oxidoreductase; Photorespiration; PhotoRDUENCE 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BC70;
Q9BC70;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bennett G.N., Koonin E.V., Smith D.K.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

EMBL; AE007524; AAK78100.1; -.

InterPro; IPR000944; UPF0074.

Pfam; PF02082; UPF0074; 1.

ProDom; PD003632; UPF0074; 1.

PROSITE; PS01332; UPF0074; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 137 AA;
                                                                                                                                                     Sargassum
                                                                                                                    -!- SIMILARITY: BELONGS TO THE RUBISCO EMBL; AF301225; AAK01554.1; -. InterPro; IPR000685; RuBisCO_large.
                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                            Phillips N., Fredericq S.; "Biogeographic and phylogenetic investigation of the pan-pacific genus "Biogeographic and phylogenetic investigation of the Gulf of Mexico Sargassum (Fucales, Phaeophyceae) with respect to the Gulf of Mexico
                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=143167;
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LARGE SUBUNIT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 RFLLKLLRKLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                              FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1.5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                  CATALYTIC ACTIVITY: D-RIBULOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLLKLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conser
Similarity 72. 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        polyceratium
                                                                                                                                                                                                                                                                                                                                                                                                                  stramenopiles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15645 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
66
             69
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8
             .28;
                                                                                                                                                                                                                                                                                                                                                                                                                 Phaeophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
  2;
  Score 36; DB Pred. No. 29; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB Pred. No. 44;
                                                            6E4CD0DCA9CE531B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C2400AA028BA5DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                   Photosynthesis
                                                                                                                                                                                                                     1,5-BISPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                               LARGE CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   Fucales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                              CRC64;
                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 137
                                                                                                                                                                                                                                                                                                                                                                                                                     Sargassaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                FAMILY
                          53
                                                                                                                                                                                                                       co(2) = 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
     Gaps
                                                                                                                                                                                                                                                                        OF
                                                                                                                                                                                                                                                                                               Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
     0
```

٠,٠

```
POPER PROPERTY OF STREET PROPERT
                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local s
Matches 8
                                                                                  Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill Brenner M., Burgess S., Hance M., Shvartsbeyn M. Riggs F., Hslao J., Zismann V., Blunt S., Pai G. Utterback T.R., Feldblyum T.V., Quackenbush J., White O., Fraser C.M.;

"Oryza sativa chromosome 10 BAC OSJNBa0010C11 ge Submitted (MAY-2001) to the EMBL/GenBank/DDBJ da EMBL, AC069300; AAK55450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q94LQ5;
01-DEC+2001
01-DEC+2001
01-DEC+2001
                                                                                                                                                                                                                     Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama Sugiyama B., Nagai K., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25415 FTS, CLONE TST03443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. NIPPONBARE;
Buell C.R., Yuan Q., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 8.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q94LQ5
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96LK7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096LK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 74 AA; 8061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
105
                                                                                                        / Match
Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ហ
                       KLLLKLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLLKLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLLLRLWLQLLK
KSLTKYLLKLLK
                                                                                     Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%;
                                                                                                          69.2%;
75.0%;
                                                                                                                                                                                                    25880
                                                                                                                                                                                                    MW;
                                                                                Score 36; DB Pred. No. 1e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB Pred. No. 38; 3; Mismatches
                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              υ
·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720EF0A677709444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                    58250E60EE1D3C5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                          DB 4;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 M., Tsitrin
i G., VanAken
J., Salzberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic sequence.";
databases.
                                                                                     Ψ
                                                                                                                             Length 237;
                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsitrin T.,
VanAken S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.N.,
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gansberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                            Chiba Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...
..
                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
```

```
RESULT
Q9G9H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Q95XU2
₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                              Ol-MAR-2001 (TrEMBLrel. 1.01-MAR-2001 (TrEMBLrel. 1.01-DEC-2001 (TrEMBLrel. 1.01-DEC-2001 (TrEMBLRel. 1.01-DEC-2001 (TREMBLRE). 1.01-DEC-2001 (TREMB
                                                                      SEQUENCE FROM N.A. MEDLINE=20377911; Pu Bullerwell C.E., Bus "A novel motif for i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q95XU2;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
HYPOTHETICAL 127.2 KDA F
                                                                                                                                                               Eukaryota; Fungi; Basidiomycota; Hymenomyce
Stereales; Schizophyllaceae; Schizophyllum.
NCBI_TaxID=5334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LLKLLLKLLK
:|||||:|:|
982 ILKLLLRLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Direct Submission.";
Submitted (NOV-2001) to the
EMBL, ACC24848; AAK68543.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                        genomes
                                                                                                                                                                                                                                Mitochondrion.
                                                                                                                                                                                                                                                Schizophyllum commune
                                                                                                                                                                                                                                                                                                                                                                                       0969н3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
Edwards J., Lamar B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nema investigating biology. The C Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y67D8A.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q95XU2
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Q9G9H3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                    Frends Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l protein
1107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                  Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                        Burger G., Lang B.F.;
or identifying rps3 homologs
                                                                                                             PubMed=10916154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . elegans
O) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; Rhabditida; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127230 MW;
                                    25:363-365(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 19, Create
1. 19, Last :
1. 19, Last :
A PROTEIN.
                                                                                                                                                                                                                                                (Bracket fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nematode C. elegans: a pl
The C. elegans Sequencing
                                                                                                                                                                                                                                                                                                          16,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cosmid Y67D8A.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; [
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation update)
                                                                                                                                                                                                              Hymenomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A27CD8BAF85A81FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107
                                                                                                                                                                                                                                                                                                                                                                                         1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kemp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲.
                                                                                                                                                                                                                                                                                                          update)
                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wohldmann
                                                                                                                                                                                                              Homobasidiomycetes;
                                                                        fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                        mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
RESULT
O64604
ID 4600
ID 700
IT 000
I
                        RESULT
Q9CP24
                                                                                                            Дb
                                                                                                                                              Qy
                                                                                                                                                                                          Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA REL RAL RAL RAL RAL RAL RAL RAL RAL SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       064604 PRELIM
064604;
01-AUG-1998 (TREMB
01-AUG-1998 (TREMB
01-BEC-2001 (TREMB
F1707.14 PROTEIN.
                                                                                                          1832
        Q9CP24
                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis A.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AC003571; AAC18812.1; -.
                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji
Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway
Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Arabidopsis thaliana
Submitted (DEC-1997) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and an evo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; A. Mitochondrion.
Mitochondrion.
1453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forget L., Ustinova J., Wang Z., Huss V.A.R., Lang F.B.F.; "Hyaloraphidium curvatum: a linear mitochondrial genome, t and an evolutionary link to lower fungi."; Mol. Biol. Evol. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL; AF402141; AAG10295.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410
                                              10
                                                                                                                                                2 LLLKLLLKLLK 12
                                                                                                                                                                                                                                                                                                                             arPro; IPR002950; Josephin.

arPro; IPR00449; UBA.

arPro; IPR0003903; UIM.

n; PF00627; UBA; 1.

n; PF02809; UIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                        LLLELMLKTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLLLKLLKLLK
|:| |||||:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVLNKLLLKILE
                                                                                                                                                                                                                                                                                                                       SM00165;
                                                                                                                                                                                        8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                   1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (TrEMBLrel. 07,
3 (TrEMBLrel. 07,
L (TrEMBLrel. 19,
    PRELIMINARY;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                UBA;
AA;
                                                                                                        1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                              69
72
                                                                                                                                                                                                                                                                                                210020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 1 BAC F1707 sequence."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170925
                                                                                                                                                                                                          . 2%;
                                                                                                                                                                                   Score 36; DB Pred. No. 6.2e 2; Mismatches
                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 8;
Pred. No. 4.9e+02;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                       6659881792E52D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C860EDB511721651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1896
263
                                                                                                                                                                               .2e+02;
1;
                                                                                                                                                                                                                              DB 10;
Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1453;
                                                                                                                                                                                                                           Length 1896;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tRNA editing,
                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O.,
A.B.,
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

4

g Q

233

KLILKQIAKILK

12 244

1 KLLLKLLKLLK

```
RESULT
Q9P184
                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PM70;

X MEDLINE-21148866; PubMed=11248100;

X MEDLINE-21148866; PubMed=11248100;

X MEDLINE-21148866; PubMed=11248100;

A May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S.

T "Complete genomic sequence of Pasteurella multocida Pm7

RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

DR EMBL; AB006058; AAK02326.1; -.

DR InterPro; IPR003593; AAA.

DR InterPro; IPR001687; ATP_GTP_A.

DR InterPro; IPR001687; ATP_GTP_A.
             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 8
    Matches
                                                                                                            SEQUENCE FROM N.A.

STRAIN=NCTC 11168;

MEDLINE=20150912; PubMed=10688204;

Parkhill J. Wren B.W., Mungall K., Ketley J.M., Churcher C.

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holro

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacte"
                                                                                                                                                                                                                                                                                                                             Q9PI84;
Q9PI84;
01-OCT-2000
                                                          reveals hypervariable sequences.",
Nature 403:665-668(2000).
EMBL; AL139075; CAB74257.1; -
Complete proteome.
SEQUENCE 318 AA; 37371 MW; E26
                                                                                                                                                                                                                                                         Campylobacter jejuni.
Bacteria, Proteobacteria,
                                                                                                                                                                                                                                    Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                   CJ0421C
                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (MEMBRANE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRUULDO, C.-.-
Pfam; PF00005; ABC_tran;
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CP24;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella multocida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEBM OR PM0242
                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LLKLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                                            |||:||||
   Similarity 58.7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L (TrEMBLrel.
L (TrEMBLrel.
L (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             60
              58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29399 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%;
88.9%;
             . . .
. . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17,
17,
19,
                                                                                                                                                                                                                                                         epsilon subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
PROTEIN.
  Score 35; DB
Pred. No. 2e+(
3; Mismatches
   ω
                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                         E26F5D88241E2968 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2DA8CAE6EE1D4FCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                   318
             2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; 1
1.7e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                   A
                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurellaceae;
                                                                                                                                                                                                                                                      Campylobacter group;
                                                                                                               Campylobacter jejuni
                      Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                      Penn C.W.,
Vliet A.H.M.,
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.S., Kapur
Pm70.";
                                                                                                                                       А.Н.М.,
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                             s,
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

```
RESULTI
OY650
ID CO
DT OO
DT OO
OC OO
RN CO
RN RD
RN RD
RN RT
RN RD
RN RT
RN RD
RN RT
RN RD
RN RT
RN RD
RN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뭐
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999
01-NOV-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             051049
051049;
01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                              OTOFERLIN.
                                                                                 Yasunaga S., Grati M., Cohen-Salmon M., El-Amraoui A., Salem N., El-Zir E., Loiselet J., Petit C.;
"A mutation in OTOF, encoding otoferlin, a FER-1-like DFNB9, a nonsyndromic form of deafness.";
mat. Genet. 21:363-369(1999).
EMBL; AFIOT/403; AAD266117.1;
EMBL; AFIOT/403; AAD266117.1;
HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A. Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., C Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hans van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., College C., Weither C., Watthey L., McDonald L., Artiach P., Bowman C., College C., Watthey L., McDonald L., Artiach P., Bowman C., College C., Watthey L., McDonald L., Artiach P., Bowman C., College C., Carlotte C., College C., Carlotte C., Carlotte
                    InterPro; IPR000008; C2. Pfam; PF00168; C2; 2. PRINTS; PR00360; C2DOMAI
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99206603; PubMed=10192385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ATCC 35210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi
Bacteria; Spirochaet
                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Y650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              091650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   burgdorferi.";
Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98065943; PubMed=9403685,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONSERVED HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003740; DUF161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLLLILIKKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02588; DUF161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            вв0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H.O., Venter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE001116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck T., Watthey L., McDonald S., Fujii C., Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conser
PR00360; C2DOMAIN
3M00239; C2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of a Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                     (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC66414.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         в31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06,
06,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                       12,
12,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s disease spiroche
Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
GRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e+
2; Mismatches
                                                                                                                                                                                                                                                                                                                          Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289D8371C6209DBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horst K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e+02;
                                                                                                                                                                                            El-Amraoui A.,
C.;
                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts K., Hatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia
                                                                                                                                                                        protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E.K., Gwinn M.,
D.,
                                                                                                                                                                                                                 Mustapha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                        causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
ID ACCOCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                   Q9HC10
                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HC09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                     Q9HC10;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9нс09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HC09
                                                                                                                                                                                                                                                                                                                                                                       15
```

```
DR
SQ
                                                                                                                                            01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-20395831; PubMed-10903124;

Wasunaga S., Grati M., Chardenoux S., Smith T.N.

Lalwani A.K., Wilcox E.R., Petit C.;

"OTOF encodes multiple long and short isoforms:

the long ones underlie recessive deafness DFNB9.

Am. J. Hum. Genet. 67:591-600(2000).

EMBL, AF183186; AAG12992.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000008; C2.
Pfam; PF00168; C2; 2.
PRINTS; PR00360; C2DOMAIN.
SMART; SM00239; C2; 3.
Yasunaga S., Grati M., Chardenoux Lalwani A.K., Wilcox E.R., Petit (
                          SEQUENCE FROM N.A. MEDLINE=20395831;
                                                               Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                 BRAIN OTOFERLIN
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00499; C2_DOMAIN_1; PROSITE; PS50004; C2_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRAIN OTOFERLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                            2 LLLKLLLKLL
||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LLLKLLLKLL
                                                                                                                                                                                                                                                                 LLLKLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTLKLLLLLL
                                                                                                                                                                                                                                                                                                                   Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00499; C2_DOMAIN_1;
PS50004; C2_DOMAIN_2;
1230 AA; 140496 MW;
                                                                                                                                                                                                                                                                                                                                                                                      1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel. )
                                                                                                                                         (TremBLrel. 16, Created)
(TremBLrel. 16, Last sequence update)
(TremBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                          PubMed=10903124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                 67.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                      148926
                                                                                                                                 ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16, Created)16, Last sequence update)19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 0 %
%
                                                                                                                                                                                                                                                                                                                   Score 35; DB
Pred. No. 6.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N N
                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
 c.;
                                                                                                                                                                                                                                                                                                                                                                                      CCCF84A6464A5462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2F0CA02F4877AB48
             s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
No.
                                                                                                                                                                                                1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1307
               Smith
                                                                                                                                                                                                                                                                                                                лв
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3e+02;
                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
            T.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.N.,
                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.
                                                                                                                                                                                                                                                                                                                                             Length 1307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic evidence that
";
                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
               Friedman
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman T.
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ъ.
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

```
Search completed: June 17, 2002, 12:44:18 Job time: 293 sec
                                                                                                                         Qy
                                                                                                                                                                                                                                            RT RT RT RT RT DR DR DR DR DR DR DR DR SQ
                                                                                                                                   Query Match 67.3%; Score 35; DB 4; Length 1997; Best Local Similarity 90.0%; Pred. No. 9.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                 2 LLLKLLLKLL 11
||||||| ||
1965 LLLKLLLLLL 1974
                                                                                                                                                                                                          "OTOF encodes multiple long and short isoforms: genetic evidence that the long ones underlie recessive deafness DFNB9.";
Am. J. Hum. Genet. 67:591-600(2000).

EMBL; AF183185; AAG12991.1; -.

INTERPROVED C2: 4.

INTERPROVED C2: 4.

PRINTS; PROVIGE; C2: C2.

PFAM; PFOVIGE; C2: C2.

PROVITE; PROVIGE; C2: 6.

PROSITE; PSOVIGE; C2-DOMAIN_2; 4.

SEQUENCE 1997 AA; 226751 MW; 24DE196371FB7385 CRC64;
                                                                                                                              0; Gaps
                                                                                                                                  0;
```

```
Mon Jun 17 15:43:12 2002
```

Title: Perfect score: Sequence: OM protein - protein search, using sw model Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-367-714A-23 52 1 KLLLKLLLKLLK 12 June 17, 2002, 12:38:20 ; Search time 34.71 Seconds (without alignments) 8.444 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Searched:

231628 seqs, 24425594 residues

231628

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: //gn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: //gn2_6/ptodata/2,
5: //gn2_6/ptodata/2,
6: //gn2_6/ptodata/2, /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

6	26	25	24	23	22	21	20	19	18.	17	16	15	14	13	12	11	10	9	6 0	7	σ	(J	4.	ω	N	_	No.	Result
ŭ	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	Score	
/3.1	76.9	76.9		76.9	6.	6	5	٠	5	6		•		9		6	76.9			٥.	ა	6		6	6	6		Query
17		36																								14	Length DB	
c c	2 US	PC	US				_																US	US		SD	BID	
-U8-944-133-13	-08-687-5	0	-07-725-331-6	PCT-US91-05047-62	6	PCT-US91-05047-61	6	US-08-290-853-19	PCT-US91-05047-60	-07-725-331-6	9	US-08-569-188-5	7019-	us-08-818-252-39	253-3	US-08-569-188-3		PCT-US94-07019-11	PCT-US94-07019-10	701	US-08-569-188-12	-08-569-188-11	-08-569-188	-08-569-188	PCT-US94-07019-8	-08-569	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
sequence 13, Appl	6, 2	e 63,	63,	62,	62,	61,	e 61,	19,	,09	60	5	5		39,	39,	Sequence 3, Appli	12,	11,	10,	Sequence 1, Appli	e 12,	11,	e 10,		ω,	Œ	Description	

Ş

1 KLLLKLLLKLLK 12

0;

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	ω L	30	29	28
35	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	3/
67.3	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2
16	18	18	18	18	18	18	18	17	17	17	17	16	16	16	16	14	14
۳	Ç	σ	4	4	4	N	ນ	ഗ	ഗ	Ν	N	ഗ	v	N	N	σ	۲
US-07-725-331-4	PCT-US94-07019-15	PCT-US94-07019-6	US-09-296-089-36	US-08-958-993A-12	US-08-960-054A-12	US-08-569-188-15	US-08-569-188-6	PCT-US94-07019-14	PCT-US94-07019-4	US-08-569-188-14	US-08-569-188-4	PCT-US94-07019-13	PCT-US94-07019-2	US-08-569-188-13	US-08-569-188-2	PCT-US91-05047-1	US-07-725-331-1
Sequence 4	Sequence 1	Sequence 6	Sequence 3	Sequence 1	Sequence 1	Sequence 1	Sequence 6	Sequence 1	Sequence 4	Sequence 1	Sequence 4	Sequence 1	Sequence 2	Sequence 1	Sequence 2	Sequence 1	Sequence 1
>	15,	6, A	36,			15,	6, A	-	4, P	14,	4 , P	13,	2, A	13,	?, A	, P	, F
Appli	Appl	Appli	Appl	Appl	Appl	Appl	\ppli	App1	λppli	, Appl	۱ppli	Appl	Appli	Appl	Appli	Appli	TIDGA

ALIGNMENTS

Query Match 76.9%; Score 40; DB 2; Best Local Similarity 83.3%; Pred. No. 1.5; Matches 10; Conservative 0; Mismatches	; SIRANDELINESS: UNKNOWN ; TOPOLOGY: Unknown ; MOLECULE TYPE: peptide US-08-569-188-8	a) E	_	, 692	; ATTORNEY/AGENT INFORMATION: ; NAME: LINDA AXAMETHY FLOYD	; FILING DATE: JUNE 22, 1993	; PRIOR APPLICATION DATA:	; CLASSIFICATION: 525	; FILING DATE:	; CURRENT APPLICATION DATA:	RD FOR WINDOWS 95	; OPERATING SYSTEM: MICROSOFT WINDOWS 95	멾	1	898	: COMMTRY: MULTINED STATES OF AMERICA	WILMINGTON	007 MARKET STREET	PONT DE NEMOURS AND	; NUMBER OF SEQUENCES: 18	WENTION: NOVEL	; APPLICANT: SHARON LPRETTA HAYNIE	; Sequence 8, Application US/08569188	RESULT 1
2;											5 (7.0)								COMPANY		COMPOSIT			
Length 14; ; Indels																		'	Κ		SNOI			
0;																								
Gaps																								

DЬ

KKLLKLLKKLLK 13

PCT-US94-07019-8

Sequence 8, Application PC/TUS9407019 GENERAL INFORMATION:

0;

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETRY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9295-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-569-188-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US94-07019-8
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08569188 Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/082,8:
APPLICATION NUMBER: 22, 1993
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARATERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                    MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
APPLICATION NUMBER: US/08/569,188
FILING DATE: US/08/569,188
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTI
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHARON I
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                           CLASSIFICATION:
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT ACTUAL NUMBER: PCT/USST/ PRIOR APPLICATION NUMBER: PCT/USST/ PRIOR APPLICATION NUMBER: 08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MACINTOSH 6.0 SOFTWARE: MICROSOFT WORD, 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKLLKLLKKLLK 13
                                                                                                                                                                                                                                                          19898
                                                                                                                                                                                                                                                                                                   WILMINGTON
                                                                                                                                                                                                                                                                                       DELAWARE
                                                                                                                                                                                                                                                                                                     E: E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                        SHARON LPRETTA HAYNIE
VENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MACINTOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.9%;
83.3%;
                                                                                                                                               US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

DЪ δÃ

1 KLLIKLLKILK 12

KKLLKLLKKLLK 15

Matches Query Match Best Local :

10;

Similarity 83.3 10; Conservative

76.98; 83.38;

Score 40; Pred. No.

DB 2;

Length 16; Indels

0; Gaps

0;

0;

Local

```
; TOPOLOGY: ur; MOLECULE TYPE: US-08-569-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-569-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.38,
Matches 10; Conservative
                                                                                                                APPLICATION NUMBER: 08/082,852
AFILING DATE: JUNE 22, 1993
ATTORNEY/AGENIT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION UMMBER: 3692
REFERENCE/DOCKET NUMBER: CR-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                            TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-569-188-1
                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 525
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                        STRANDEDNESS:
                                              LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1007 MARI
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10, Application US/08569188
5. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                           DELAWARE
                          unknown
                                                                                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHARON LPRETTA HAYNIE
            peptide
                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.9%;
83.3%;
                                                                                                                                                                                                                  08/082,852
                                                                                                                                                                                                                                                                     US/08/569,188
                                                                                                                                             CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
```

```
US-08-569-188-12

; Sequence 12, Application US/08569188

; Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                            ·Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: ur; MOLECULE TYPE: US-08-569-188-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-569-188-11
                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Mätch
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08569188 Patent No. 5847047
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 11:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: LOU,
CITY: WILMINGTON
CTATE: DELAWARE
TMITTED S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFÉRENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPEAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: JUNE 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                  APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
                                                                                                                                       STREET: 1007 MAKE
CITY: WILMINGTON
                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                KKLLKLLKKLLK 15
                                                                                           19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i: 16 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19898
                                                                                                                          DELAWARE
                                                                                                                                                        E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHARON LPRETTA HAYNIE
VENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                         UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
```

```
δã
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-569-188-12
                                                                                                                         PCT-US94-07019-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US94-07019-1
                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                     APPLICATION NUMBER: 08
FILING DATE: JUNE 22,
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                      COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/070
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOS:
TITLE OF INVENTION: COMPOS:
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: LINDA AXAMETHY FLOYD REGISTION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                    TOPOLOGY: ui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                             LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
           1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLLLKLLKLLK 12
KKLLKLLKKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9407019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 amino acids
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUNE 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                  76.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                     NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/082,852
                                                                                                                                                                                                                                               08/082,852
                                                                                                                                                                                                                                                                           PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR-9295-A
                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
                                                                   Pred.
                                                                            Score 40;
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                   No.
                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                               Length 16;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
```

RESULT 8 PCT-US94-07019-10; Sequence 10, App

Application PC/TUS9407019

SENERAL INFORMATION:

TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:

NOVEL ANTIMICROBIAL COMPOSITIONS

```
RESULT 10
PCT-US94-07019-12
                                                                B
                                                                                          Qγ
                   RESULT
                                                                                                                                                                                                  PCT-US94-07019-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
PCT-US94-07019-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                Query Match 76.9%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US94-07019-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 83:

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                       FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/07
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBERS
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL ANTIMICROBIAL TITLE OF INVENTION: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                        4 KKLLKLLKKLLK 15
                                                                        1 KLLLKLLKLLK 12
| ||||| ||||
                                                                                                                                                                                                                                           LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACINTOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                        MACINTOSH 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                 08/082,852
                                                                                                                                                                                                                                                                                                                                                               PCT/US94/07019
                                                                                                                           Score 40; DB 5;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No. 1
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 16;
                                                                                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

```
RESULT 11
US-08-569-188-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЪ
                                                            PRIOR APPLICATION NUMBER: 08/082,852
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
ATTORNEY/ACENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 3,692
REFERENCE/DOCKET NUMBER: CR-9295-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CT-US94-07019-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08569188 Patent No. 5847047
                                 TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.9%;
Best Local Similarity .83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MACINTOSH 6.0 SOFTWARE: MICROSOFT WORD, 4.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/0701: PRIOR APPLICATION NUMBER: 08/082,852 FILING DATE: JUNE 22, 1993
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: JUNE 22,
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
APPLICATION NUTEER DATA:
APPLICATION NUTEER DATA:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 525
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1007 MARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MASOFTWARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             19898
                                                                                                                                                                                                                                                                                                                                                                                                                             DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: E. I. DU PONT D
                                                                                                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHARON LPRETTA HAYNIE
FINTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                            US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 5;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
```

0;

```
RESULT 13
US-08-818-252-39
; Sequence 39, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
                                                                                                                             밁
                                                                                                                                                        Q
                                                                                                                                                                                                                                                                      ; TOPOLOGY: li;; MOLECULE TYPE: US-08-818-253-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-569-188-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-818-253-39
                                                                                                                                                                                                                                                                                                                     AFFLIA DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0725
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-509
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/08818253 Patent No. 5998204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.9%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsien, KOYEL ...
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: unknown TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KKLLKLLKKLLK 16
                                                                                                                           4 KKLLKLLKKLLK 15
                                                                                                                                              1 KILLKLLKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92037
R 92037
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                        76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Windows 95
                                                                                                                                                                                       Score 40; DB 2
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                     07257/043001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 2;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0b
                                                                                                                                                                                                                       2;
                                                                                                                                                                                       2;
                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                         0
                                                                                                                                                                                           밁
                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뮹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                           US-08-569-188-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US94-07019-3
                                                                                                                                                                                                                                                                                                                                     PCT-US94-07019-3
                                                                                        Sequence 5, Application US/08569188 Patent No. 5847047
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                     Query Match
                                                            GENERAL INFORMATION: APPLICANT: SHARON
           TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                       10;
                                                            SHARON LPRETTA HAYNIE
```

```
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: TOTHER INFORMATION: Calmodulin binding peptide-2 US-08-818-252-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Watches 10; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           TENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                      SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/070
PRIOR APPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL A TITLE OF INVENTION: COMPOSI NUMBER OF SEQUENCES: 15 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
              1 KLILKLLKLLK 12
5 KKLLKLLKKLLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLLKLLK 12
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      MACINTOSH
                                                                                76.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                    PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                Score 40; DB 5; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 4; Pred. No. 1.8;
                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                  Length 17;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                Gaps
```

```
COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 95

SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188

FILING DATE:
CLASSIFICATION NUMBER: 08/082,852

PRIOR APPLICATION NUMBER: 22,193

APPLICATION NUMBER: 22,193

ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION UNUMBER: 33,692

REFERENCE/DOCKET NUMBER: CR-9295-A

TELEPOMMUNICATION INFORMATION:
TELEPIAN: 302-892-8112

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TTYPE: amino acids
STRANDEDNESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
US-08-569-188-5
Search completed: June 17, 2002, 12:42:03 Job time: 223 sec
                                                                                                                                                                                                  Query Match 76.9%; Score 40; DB 2; Length 18; Best Local Similarity 83.3%; Pred. No. 1.9; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                       1 KILLKILKKIK 12
| |||| |||
6 KKILKILKKILK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 11007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
                                                                                                                                                                                               2; Indels
                                                                                                                                                                                               0;
                                                                                                                                                                                             Gaps
                                                                                                                                                                                             0;
```

Ъ Qy

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
   5
10
11
11
                                                                                                                                                                                                                                                                                                               Pred. Nescore cand is
                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq
                                                                                                                                                                                                                                                                                                                                greater
                                                                                                                                                                                                                                                                                                                 derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to havater than or equal to the score of the result being rived by analysis of the total score distribution.
   100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_032802:*

1. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

3. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

3. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

4. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

5. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*

6. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*

7. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*

8. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       June 17, 2002, 12:41:21; Search time 94.14 Seconds (without alignments) 7.079 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-367-714A-28
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/yeneseqp-embl/AA1988.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
                                                                                                                                                                                                                       Length
   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapext 0.5
   118
119
119
119
119
119
119
119
                                                                                                                                                                                                                        IJ
AAW35154
AAW82852
AAB17418
AAW45766
AAW45766
AAW45166
AAW35166
AAW35166
AAW35167
AAW177384
AAW177384
AAW45767
                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747574
             Leu/Lys diastereom
Antipathogenic pep
Antipathogenic pep
Antipathogenis pep
KL-4 pulmonary sur
KL-4 pulmonary sur
Leu/Lys diastereom
Antipathogenic pep
Antipathogenic pep
Antipathogenic pep
KL-4 pulmonary sur
Lytic peptide with
                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                have
                                                                                                                                                                                                                                                                                                                            printed,
```

22444	2222222	, , , , , , , , , , , , , , , , , , ,) N N N N N N N N N N N N N N N N N N N
		. <i></i>	110000.0000.00000.00000.00000.000000.00000
145 145 187 187 187	2431 2431 16 43 80	133 136 171 197 197 258 259 307	11112 1112 1122 1122 1122 1235 134 135 135 135 135 135 135 135 135 135 135
221	113	21 21 22 22 22 22 22 22 22 22 22 22 22 2	14 14 18 19 19 19 19 19 19 19 19
AAU21748 AAU21748 AAY66677 AAU29236 AAB85575	AAG46587 AAG46587 AAW25138 AAW177285 AAW17726 AAW28160 AAW28160	AA00228 AA013335 AA037473 AA055601 AA055599 AA055599 AA065599	AAR30661 AAW32109 AAW45763 AAW82278 AAB48039 AAB49683 AAB49683 AAB46100
Novel human enzyme Novel human neopla Membrane-bound pro Human PRO polypept Human glutathione	dopsis non-str philic human acid s	Human polypeptide Human polypeptide Amino acid sequenc Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia	9 0 0 0 PH 0 0 0 0

ALIGNMENTS

AAW35154 RESULT

μ,

AAW35154 standard; peptide;

σ Ą

14-APR-1998 AAW35154;

(first entry)

Oren Z, Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis agricultural pesticide; cell wall lysis. Misc-difference Synthetic Leu/Lys diastereomer (YEDA) YEDA RES & DEV CO LTD 22-FEB-1996; 20-FEB-1997; 28-AUG-1997 WO9731019-A2 Misc-difference Shai Y; 96IL-0117223. 97WO-IL00066. Location/Qualifiers /note= /note= "D-form residue" peptide [D]-L1,3-K2L4. "D-form residue bacterial cell lysis;

```
RESULT
AAW82852
ID AAW8
XX AAW8
AC AAW8
XX 19-W
XX ANTI
XX Non-
KW Canc
KW Canc
KW Canc
KW WO98
AX 27-A
XX 19-F
YX 20-F
XX 20-F
XX WPI;
XX WPI;
XX New
PT infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC This sequence represents a Leu/Lys diastereomer peptide of the CC invention. The peptides of the invention have: (a) cytolytic activity on the peptides of the invention have: (a) cytolytic activity on the cells (pathogenic cells (pathogenic and malignant cells not naturally present in CC concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as concernatives for food, cosmetics and agricultural produce, or as concernative for food, cosmetics and agricultural produce, or as concernative for protocolated structures) means that the peptides concernative for particular structures means that the peptides concernative descriptions concernations concluded by the concernation of alpha-helical structures) means that the peptides concernative for protocolated by the concernation of alpha-helical structures of the concernation of alpha those that include D-aa will have concernated are sistance to protocolytic degradation. Non-haemolytic, concernation of alpha-helical structures are pecific spectrum of these random copolymers of pardaxin, each has a specific spectrum of these random copolymers induce total lysis of bacterial cell walls, xx resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
      New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                        WPI; 1998-594464/50
                                                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                       Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                           20-FEB-1997;
                                                                                                                                                                                                                                              19-FEB-1998;
                                                                                                                                                                                                                                                                                    27-AUG-1998
                                                                                                                                                                                                                                                                                                                        W09837090-A1
                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW82852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW82852 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide(s) having selective cytolytic activity - again and malignant cells, but no haemolytic activity, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 k1111k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                 Shai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 40; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                       97WO-IL00066.
                                                                                                                                                                                                                                            98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4e+05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against pathogens used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

0;

```
AAB17418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
""" 6; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC The present peptide is used to produce the agents of the invention. The CC specification describes a non-haemolytic, cytolytic agent, which is a CC peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copplymer. The agent has a sclective cytolytic activity on CC pathogenic cells. The agent has a sclective greater than 1, comprises L-amino CC peptide which has a net positive charge greater than 1, comprises L-amino acid residues and comprises an alpha-helix CC comprises L-amino acid residues and comprises an alpha-helix CC comprises L-amino acid residues and presidues, has a net CC comprises L-amino acid residues and presidues, has a net CC is not found in nature. The cytolytic agents may be used for treatment of concluding bacterial, fungal, viral, mycoplasma and protozoan infections. CC They may be used in both human and veterinary medicine. They may also be cosmetic and food industries, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries, as pesticides (e.g. fungicides or CC cosmetic and food industries as pesticides (e.g. fungicides or CC cosmetic and food industries as pesticides (e.g. fungicides or CC cosmetic and food industries as pesticides (e.g. fungicides or CC cosmetic and food industries as pesticides (e.g. fungicides or CC cosmetic and food industries as pesticides (e.g. fungicides or CC cosmetic and food industries as pesticides (e.g. fungicides or CC cosmetic and cosmetic and food industries as pesticides (e.g. fungicides or CC 
           Novel composition of matter comprising an pharmacologically active peptides, useful autoimmune diseases -
                                                                                                          WPI; 2000-350702/30
                                                                                                                                                                                                                                              23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                           04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMP; inhibitor; erythropoietin; cytotoxic T cell lymphocyte ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antipathogenic peptide sequence SEQ ID NO:522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17418 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 klllllk 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Page 106; 126pp; English.
                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 26; DB 19; ilarity 100.0%; Pred. No. 6.4e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã,
                                                                                                                                                                                                                                              98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                              99WO-US25044
                                                                                                                                                       Cheetham
                                                                                                                                                    ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                    Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin 1;
ecrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
```

0;

Fc domain and for treating ,

cancer

and

Claim 39;

Page 379;

608pp; English.

is

```
RESULT
AAW45766
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of
             Abdel-magid AF,
Villani FJ;
                                                                                      17-JUL-1996;
                                                                                                                  11-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                 Liquid phase peptide synthesis; KL-4 pulmonary surfactant coupling; respiratory distress syndrome; saponification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
                                                                                                                                                22 - JAN-1998
                                                                                                                                                                            WO9802461-A2
                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                coupling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KL-4 pulmonary surfactant protein precursor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW45766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW45766 standard; peptide; 8
                                                         (ORTH ) ORTHO PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLLK 6
1 kllllk 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                     96US-0021455
                                                                                                                  97WO-US12163
                           Eggmann U,
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                         /note≖
                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                         "N-terminally modified by t-butyloxycarbonyl group. Side chain amino group protected by
                                                                                                                                                                                                      "Leu-OR, where R is 1-8C alkyl or phenyl 1-8C alkyl"
                                                                                                                                                                                                                                                                   "Side chain amino
                                                                                                                                                                                                                                                Side chain amino group of Lys6 protected by benzyloxycarboxyl group"
                                                                                                                                                                                                                                                                                            group. Side chain amino
benzyloxycarbonyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                           Maryanoff CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
6.4e+05;
thes 0;
                          Thaler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

```
CC This peptide is used in a novel process for the synthesis of a KL-4 CC pulmonary surfactant protein. The process comprises: (a) reacting a CC 3-amino acid peptide residue of formula H-Lys(2)-Leu-Leu-OH with a 5-CC amino acid peptide residue Boc-Leu-Leu-OH with a 5-CC amino acid peptide residue Boc-Leu-Lys(2)-Leu-Leu-OH (II) to yield CC an 8-amino acid peptide residue, which is successively reacted with the CC 5-amino acid peptide to form an 18-amino acid peptide of formula H-Leu-Leu-CC Lys(2)-Leu4)3Lys(2)-OBzl (IIIa); (b) reacting the 18 amino acid CC peptide with a 3-residue amino acid peptide of formula H-Leu-Leu-CC Lys(2)-OBzl (X) to form the protected 21-amino acid KL-4 protein; and CC reaction with a suitable acid to form the final KL-4 protein. The CC methods can be used for the preparation of the polypeptide component of the synthetic pulmonary surfactant KL-4 which can be used in the CC treatment of respiratory distress syndrome. The saponification process CC can provide for the deprotection of a peptide ester protected carboxyl Group with reduced racemisation. The liquid phase peptide processes CC provide advantages in solubility and control over unwanted by-products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 27; 30pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-110531/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
```

```
Query Match
Best Local
                                                      Local Similarity
                       1 KLLLLK 6
1 | | | | | | 6
1 kllllk 6
ហ
                                                       Conservative
                                                             100.0%;
                                                       0,:
                                                            Score 26;
Pred. No.
                                                       Mismatches
                                                           ; DB 19;
. 6.4e+05;
                                                       0
                                                                    Length
                                                       0;
                                                     Gaps
```

0

밁 Qy

Sequence

8 AA;

```
Ħ
                                                                                                                                        AAW45768
Liquid
                               KL-4 pulmonary
                                                             19-JUN-1998
                                                                                            AAW45768
                                                                                                                        AAW45768 standard; peptide; 8 AA
                                                            (first entry)
                               surfactant protein precursor peptide
```

```
17-JUL-1996;
                        11-JUL-1997;
                                         22-JAN-1998.
                                                         WO9802461-A2
                                                                                                     Modified-site
                                                                                                                             Modified-site
                                                                                                                                                                                Synthetic
                                                                                                                                                                                               coupling;
                                                                                                                                                       Modified-site
                                                                                                                                                                                                phase peptide synthesis; KL-4 pulmonary surfactant protein;
ng; respiratory distress syndrome; saponification.
        96US-0021455
                         97WO-US12163
                                                                                                    8
                                                                                                                              ω
                                                                                            /note=
                                                                                                                     /note=
                                                                                                                                             /note=
                                                                                                                                                              Location/Qualifiers
                                                                                                                                    "N-terminally modified by t-butyloxycarbonyl group"
                                                                                           "Side chain amino group of Lys8 protected
                                                                                                          "Side chain amino group of Lys3 benzyloxycarboxyl group"
                                                                          benzyloxycarboxyl group. C-terminally modifed by OBzl"
                                                                                                                    protected
```

```
RESULT
AAW35166
                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This peptide is used in a novel process for the synthesis of a KL-4 CC 3-amino acid peptide residue of formula H-Lys(Z)-Leu-Leu-OH with a 5-CC amino acid peptide residue Boc-Leu-Lys(Z)-Leu-Leu-OH with a 5-CC an 8-amino acid peptide residue, which is successively reacted with the CC H-Leu-Leu(Lys(Z)-Leu-Leu-OH (II) to yield CC 5-amino acid peptide to form an 18-amino acid peptide of formula CC H-Leu-Leu(Lys(Z)-Leu-Leu-OH (II) to yield CC H-Leu-Leu(Lys(Z)-Leu-Leu-OH (III)) to yield CC H-Leu-Leu(Lys(Z)-Leu-Leu-OH (III)) to yield CC H-Leu-Leu(Lys(Z)-DBZ1 (IIIa); (b) reacting the 18 amino acid CC H-Leu-Leu-OH (III) to yield CC H-Leu-Leu-OH (III) to yield IIIa); (b) reacting the 18 amino acid CC Lys(Z)-OBZ1 (X) to form the protected 21-amino acid KL-4 protein; and CC reaction with a suitable acid to form the final KL-4 protein. The CC methods can be used for the preparation of the polypeptide component of the synthetic pulmonary surfactant KL-4 which can be used in the CC treatment of respiratory distress syndrome. The saponification process group with reduced racemisation of a peptide ester protected carboxyl provide advantages in solubility and control over unwanted by-products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
W09731019-A2
                                                              Misc-difference
                                                                                         Misc-difference
                                                                                                                    Misc-difference
                                                                                                                                               Misc-difference
                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                 Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                           Leu/Lys diastereomer peptide [D]-L3,4,8,10-K3L9.
                                                                                                                                                                                                                                                                                                                      14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                   AAW35166 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                 AAW35166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2a; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-110531/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abdel-magid AF,
Villani FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ORTH ) ORTHO PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                 /note=
10
                                       /note= "D-form residue"
12
                                                                                                                                                  Location/Qualifiers
                                                                                                      /note=
                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eggmann U,
               "C-terminal amide"
                                                                       "D-form
                                                                                                "D-form residue"
                                                                                                                          "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DE
Pred. No. 6.4
0; Mismatches
                                                                       residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maryanoff CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
6.4e+05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thaler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                             bacterial cell lysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
```

```
DT
XX
DE
XX
XX
XX
XX
XX
PN
PD
PD
XX
XX
XX
PPR
                                                                                                                                                                                                                                                                                  AAW82883
ID AAW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                            γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a Leu/Lys diastereomer peptide of the CC invention. The peptides of the invention have: (a) cytolytic activity on the body, but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protozoa, mycoplasma or viruses) created the concentratives for food, cosmetics and agricultural produce, or as concentratives for food, cosmetics and agricultural produce, or as concentratives for food, cosmetics and agricultural produce, or as concentrative for food, cosmetics and agricultural produce, or as concentrative for fany toxic effects, and those that include D-ta will have concentrated the protocolymers of pardaxin, each has a specific spectrum of these random copolymers of pardaxin, each has a specific apportant of these random copolymers induce total lysis of bacterial cell walls, xx
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 6
        20-FEB-1997;
                                 19-FEB-1998;
                                                                                     W09837090-A1
                                                                                                                                    Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                                         Antipathogenic peptide
                                                                                                                                                                                                                         19-MAY-1999
                                                                                                                                                                                                                                                      AAW82883;
                                                                                                                                                                                                                                                                      AAW82883 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide(s) having selective and malignant cells, but no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3;
                                                                                                                                                                                                                                                                                                                                                7 klilik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                         1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1997
                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 39;
    97WO-IL00066
                             180001I-0M86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-IL00066.
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80pp; English.
                                                                                                                                  fungicide; bactericide
                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytolytic activity - against pathogens haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veteriary medicine. They may also be
               23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                        cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used as disinfectants for destruction of microorganisms, i.e. solutions for wetting contact lenses, as preservatives, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification describes a non-haemolytic, cytolytic agent, which is peptide, a complex of bundled peptides, a mixture of peptides or a peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present pe
specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                  W0200024782-A2
                                                                                                                                             Synthetic
                                                                                                                                                                            asthma;
                                                                                                                                                                                                                                                                                                                        31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3;
                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                          Antipathogenic peptide sequence SEQ ID NO:516.
                                                                                                                                                                                                                                                                                                                                                       AAB17412
                                                                                                                                                                                                                                                                                                                                                                                AAB17412 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bactericides) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cosmetic and food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                               .
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                          thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 38; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
               98US-0105371.
99US-0428082.
                                                        99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ę٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     industries, as pesticides (e.g. for preservation of agricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 င
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTD.
                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  produce the agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                   antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each CC independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)e-P3-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW45767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                     coupling;
                                                                                                                                                                                                                                                                                                                                                                                            KL-4 pulmonary surfactant protein precursor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW45767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW45767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 39; Page 377; 608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U,
                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                        Liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention
                                                                                                                             Modified-site
                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 kllllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                       respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                     peptide synthesis; KL-4 pulmonary surfactant protein;
spiratory distress syndrome; saponification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ξ,
                                                                        13
                                                                                                                             œ
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                    /note=
                                                                                                         /note=
                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 describes composition of matter (I) comprising gically active peptides, and linkers. Where (I)
                               "Side chain amino group of Lys13 protected benzyloxycarboxyl group. C-terminally
                                                                                                                                             "Side chain amino group of
benzyloxycarboxyl group"
                                                                                                         "Side
                                                                                                                                                                                                                         "N-terminally
             benzyloxycarboxyl modifed by OBzl"
                                                                                        Side chain amino benzyloxycarboxyl
                                                                                                                                                                                                     group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TC;
                                                                                                                                                                                                                       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
17;
                                                                                    group of group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fc domain
for treati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                         уd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                       t-butyloxycarbonyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12
                                                                                                       Lys8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                         protected
                                                                                                                                                                protected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                         þу
                                                    γģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an
is:
```

W09802461-A2

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                 This peptide is used in a novel process for the synthesis of a KL-4 CC pulmonary surfactant protein. The process comprises: (a) reacting a CC 3-amino acid peptide residue of formula H-Lys(Z)-Leu-Leu-OH with a 5-CC an 8-amino acid peptide residue Boc-Leu-Lys(Z)-Leu-Leu-OH (II) to yield CC an 8-amino acid peptide to form an 18-amino acid peptide of formula CC H-Leu-Leu(Lys(Z)-Leu4)3Iys(Z)-OBZ1 (IIIa); (b) reacting the 18 amino acid compensation acid peptide of formula CC Lys(Z)-OBZ1 (XI) to form the protected 21-amino acid KL-4 protein; and CC reaction with a suitable acid to form the 21-amino acid KL-4 protein by CC compensation of the polypeptide component of treatment of respiratory distress syndrome. The saponification process can provide for the deprotection of a peptide ester protected carboxyl provide advantages in solubility and control over unwanted by products.
                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                Matches
WO9841535-A2
                              Modified-site
                                                                                              Biologically active peptide; hormone; drug; toxin; lipid bilayer membrane; microorganism; parasite; v
                                                                                       Synthetic.
                                                     Modified-site
                                                                                                                                    Lytic peptide with alterable function
                                                                                                                                                                  14-DEC-1998
                                                                                                                                                                                         AAW77384;
                                                                                                                                                                                                     AAW77384 standard; peptide; 15
                                                                                                                                                                                                                                                                  1 KLLLLK 6
|||||
3 kllllk 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide
                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-110531/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abdel-magid AF,
Villani FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ORTH ) ORTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 25; 30pp; English.
                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                             (first entry)
                /note=
15
/note=
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9608-0021455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US12163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eggmann U,
              "C-terminal
                                "Optional N-terminal
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                Score 26; DB
Pred. No. 18;
                                                                                                                                                                                                        AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maryanoff CA,
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                     9
                                                                                                 parasite; virus
                               myristyl'
                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thaler
                                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                             0,
```

```
RESULT 11
                                                                                                                                                                                                                                                                                                                AAW45765
                                                                                                                                                                                                                                                                                                                                                          Ъ
                                                                                                                                                                                                                                                                                                                                                                            ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                             Modified-site
                                                                            Modified-site
                                                                                                            Modified-site
                                                                                                                                                                                  Liquid phase peptide synthesis; KL-4 pulmonary surfactant protein; coupling; respiratory distress syndrome; saponification.
                                                                                                                                            Modified-site
                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                       KL-4 pulmonary surfactant protein precursor peptide.
                                                                                                                                                                                                                                                       19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The peptides AAW7376-W77390 can be modified by the method of the invention by substituting at least one amino acid of the peptide to provide a peptide having at least one amino acid which is modifiable by acids which are not modifiable by the reaction in the peptide with amino drugs, toxins and peptides which act on lipid bilayer membranes. The parts in order to affect the structure or integrity or permeability of a body of the animal or plant or within the cells of the body of the animal or plant or within the cells of the body of the animal or plant or within the cells of the body of the animal or plant or within the cells of the body of the animal
                                                                                                                                                                                                                                                                              AAW45765;
                                                                                                                                                                                                                                                                                          AAW45765 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                     1 KLLLLK 6
|||||
| kllllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified peptide(s) - obtained by substitution with an acid which is modifiable by a reaction and replacing other acids which are not to be modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 13; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-521161/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ANMA-) ANMAT TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ajoula HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clarke DJ;
                                             18
                                                                             13
                                /note=
                                                                                                              α
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                 /note=
                                                                                                 /note=
                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97GB-0005519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-GB00799
"Side chain amino group of Lys protected benzyloxycarboxyl group and C-terminus modifed by \mathsf{OBz1} "
                                                                                                        "Side chain amino group of Lys protected benzyloxycarboxyl group"
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 26; DB 100.0%; Pred. No. 21; tive 0; Mismatches
                                                "Side chain amino obenzyloxycarboxyl
                                                                                "Side chain amino denzyloxycarboxyl
                                                                                                                                                                                                                                                                                             A
                                                                               group of
                                               group of
                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                       Lys
                                                                                       Lys
                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                      protected
                                                                                      protected
                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino
                     γď
                                                     bу
                                                                                                                     ьy
                                                                                                                                                                                                                                                                                                                                                                                Gaps
```

```
RESULT
AAR30661
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-Leu-Leu(Lys(2)-Leu4)3Lys(2)-OBzl (IIIa); (b) reacting the 18 amino acid peptide with a 3-residue amino acid peptide of formula H-Leu-Leu-Lys(2)-OBzl (X) to form the protected 21-amino acid KL-4 protein; and (c) removing the protecting group of the 21-amino acid KL-4 protein by reaction with a suitable acid to form the final KL-4 protein. The methods can be used for the preparation of the polypeptide component of the synthetic pulmonary surfactant KL-4 which can be used in the treatment of respiratory distress syndrome. The saponification process can provide for the deprotection of a peptide ester protected carboxyl group with reduced racemisation. The liquid phase peptide processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pulmonary surfactant protein. The process comprises: (a) reacting a 3-amino acid peptide residue of formula H-Lys(2)-Leu-Leu-OH with a 5-amino acid peptide residue Boo-Leu-Leu-Hys(2)-Leu-Leu-OH (II) to yield an 8-amino acid peptide residue, which is successively reacted with the 5-amino acid peptide to form an 18-amino acid peptide of formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1a; Page 25; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-1997;
           01-JUN-1992;
                                                                                           Synthetic
                                                                                                                                   Pulmonary
                                                                                                                                                             Peptide
                                                                                                                                                                                          13-MAY-1993
                                                                                                                                                                                                                                               AAR30661 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of KL-4 pulmonary surfactant - using liquid phase peptide synthesis procedures by coupling appropriate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-110531/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ORTH ) ORTHO PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09802461-A2
                                     23-DEC-1992.
                                                                                                                                                                                                                     AAR30661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provide advantages in solubility and control over unwanted by-products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abdel-magid
                                                                                                                                                                                                                                                                                                                  1 KLLLLK 6
111111
3 kllllk 8
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                           1:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide is used in a novel process for the synthesis of a KL-4
                                                                                                                                                             contg.
                                                                                                                                   surfactant;
                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑF,
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                        (first entry)
                                                                                                                                                             alternating hydrophobic and hydrophilic regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0021455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US12163
          92WO-US04537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eggmann
                                                                                                                                                                                                                                               peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                  phospholipid; respiratory distress syndrome;
                                                                                                                                                                                                                                                                                                                                                                                       . 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maryanoff CA,
                                                                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No.
                                                                                                                                                                                                                                               Å
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thaler
                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                         0;
```

```
RESULT 1
AAW32109
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptide is an example of a highly generic peptide comprising 10 60 amino acid residues, including a sequence having alternating hydrophobic and hydrophilic amino acid residue regions. When the polypeptide is mixed with a phospholipid a synthetic pulmonary surfactant is formed which has greater surfactant activity than the phospholipid alone. The surfactant is used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide(s) comprising alternating hydrophobic and hydrophilic residue regions - are useful as pulmonary surfactants for treating respiratory distress syndrome
                                                                                                                                                                                                                                                                                              Liposomal pulmonary surfactant composition; preparation; respiratory distress syndrome; premature infant; premature monolayer formation; alveolar air-water interface.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW32109 standard; peptide;
                                Claim 3; Page 16; 31pp; English.
                                                                  Improved preparation of liposomal pulmonary surfactant - for
treatment of respiratory distress syndrome in premature infants
                                                                                                      WPI; 1997-298058/27.
                                                                                                                                                                            20-NOV-1995;
                                                                                                                                                                                                  22-OCT-1996;
                                                                                                                                                                                                                         29-MAY-1997
                                                                                                                                                                                                                                                 WO9719108-A1
                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                            Liposomal pulmonary surfactant composition polypeptide.
                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                           AAW32109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phospholipid alone. The surfactant respiratory distress syndrome (RDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-017902/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1991;
                                                                                                                                                  (ORTH ) ORTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLLK 6
|||||
6 kllllk 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR30655-64
                                                                                                                             Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                    PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91US-0715397
                                                                                                                            Sampino K,
                                                                                                                                                                            95US-0007347
                                                                                                                                                                                                 96WO-US16804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0%;
                                                                                                                             Weber JV;
                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-
```

The preparation of liposomal pulmonary surfactant composition ethanolic injection has been improved. The liposomal pulmonary

ьy

```
RESULT 1
AAM45763
ID AAM4
XX AAM4
AC AAM4
AC AAM4
AC II-J
XX I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
Matches
                                                                                                                                                                                   Claim la; Page 25;
                                                                                                                                                                                                                             Preparation of KL-4 pulmonary surfactant peptide synthesis procedures by coupling
                                                                                                                                                                                                                                                                                          WPI; 1998-110531/10.
                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                               (ORTH ) ORTHO PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9802461-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coupling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KL-4 pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW45763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW45763 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                       sequence represents a synthetic KL-4 pulmonary surfactant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . klilik 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phase peptide synthesis; KL-4 pulmonary surfactant protein;
ng; respiratory distress syndrome; saponification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                         AF, Eggmann U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                96US-0021455
                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US12163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surfactant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                             30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                       Maryanoff CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches

    using liquid phase
appropriate peptide

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                   Thaler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
```

0,

0

.

acid

```
pulmonary surfactant of the invention. It is a mimic of human

Surfactant protein SP-18. Synthetic pulmonary surfactants comprise

one or more phospholipids and a peptide having alternating

charged and uncharged amino acids (see AAW82728-82 and AAW88193-97).

The synthetic pulmonary surfactant is used in a claimed method for

pulmonary lavage of a mammal. Lavage is used to treat respiratory

contents, pulmonary inflammation or infection, acute hypoxaemia,

persistent foetal circulation, congenitad diaphramatic hernia,

persistent foetal circulation, inhalation of hot or noxious vapour,

persistent foetal circulations. The lavage solution removes

inflammatory mediators and preserves or restores pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW82278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9999999998<del>%</del>&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                     KL4 is a synthetic peptide that can be used in a synthetic pulmonary surfactant of the invention. It is a mimic of human
                                                                                                                                                                                                                                           Claim 44; Page 123; 145pp;
                                                                                                                                                                                                                                                               Pulmonary lavage with dilute surfactant solution at positive end-expiratory pressure - with removal of fluid using short periods of suction, used to treat respiratory distress, e.g. in neonates where caused by aspiration of meconium
                                                                                                                                                                                                                                                                                                                                                                                          Cochrane CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surfactant; pulmonary lavage; inflammation; acute hypoaemia; diaphramatic hernia; respiratory distress syndrome; meconium aspiration syndrome; pneumonia; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09849191-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surfactant peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lys(2)-OBzl (X) to form the protected 21-amino acid KL-4 protein; and (C) removing the protecting group of the 21-amino acid KL-4 protein by reaction with a suitable acid to form the final KL-4 protein. The methods can be used for the preparation of the polypeptide component of the synthetic pulmonary surfactant KL-4 which can be used in the treatment of respiratory distress syndrome. The saponification process can provide for the deprotection of a peptide ester protected carboxyl group with reduced racemisation. The liquid phase peptide processes provide advantages in solubility and control over unwanted by-products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW82278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW82278 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 k1111k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                         1999-034654/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                       Revak SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0848580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US01711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KL4
                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB
Pred. No. 31;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
```

```
CC function.

XX

SQ Sequence 21 AA;

SQ Sequence 21 AA;

Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLLLK 6
| | | | | | |
Db 1 kllllk 6

Search completed: June 17, 2002, 12:41:22

Job time: 297 sec
```

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Com
    Compugen Ltd
```

OM protein - protein search, using sw model

Run on: June 17, 2002, 12:42:57; Search time 46.42 Seconds (without alignments) 12.420 Million cell updates/sec

Title: Perfect score: US-09-367-714A-28 26

1 KLLLLK 6

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0, Gapext 0.5

283138 seqs, 96089334 residues

Searched:

Total number of hits satisfying chosen parameters: 283138

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir3:* pir2:* pir1:*

Database :

PIR_71:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	o	υ	4	ω	2	_	No.	Result
24	24	24	24	24	24	24	24	24	24	24	24	26	26	26	26	26	26	26	26	26	26	26	- 26	26	- 26	26	26	26	Score	-
92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match	Query
239	217	217	215	215	201	165	146	95	93	80	41	2431	1855	748	688	641	809	542	542	403	392	321	. 305	277	205	126	110	110	Length	
N	N	μ.	N	N	N	N	N	N	N	N	N	_	N	N	ν	N	N	2	N	N	Ν	N	N	N	N	N	2	2	BB	
T41951	H71912	B64600	G71537	A81693	AG1668	A64227	C81036	E95270	S15948	н84974	T07329	MNWVSF	S41649	A60202	S32961	A39961	T18437	E81105	B81910	B71482	A81745	S51395	A70212	AB2461	C87309	B72621	F81868	A47154	Ħ	
hypothetical prote	probable oxidoredu	NĀD(P)H-flavin oxi	hypothetical prote	ס		hypothetical prote	Z					nonstructural poly	DNA polymerase - m	choline O-acetyltr	hypothetical prote	choline O-acetyltr	hypothetical prote	ABC transporter, A	٠	hypothetical prote	~	hypothetical prote		hypothetical prote		cal prot	┰.	ב	Description	

4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3
389	387	386	356	352	346	337	333	330	328	325	294	262	260	244	239
N	N	ພ	N	Н	2	2	Ν	N	N	N	N	N	Ν	2	2
АН3003	T26735	D42528	T06756	E71092	T13837	T18708	AB2130	AD2082	H75073	T31977	T19055	A99155	E90010	T30358	A81301
penicillin-binding	hypothetical prote	B23R protein - vac	hypothetical prote	hypothetical prote	NADH dehydrogenase	hypothetical prote	iron(III) dicitrat	iron(III) dicitrat	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	probable anion-upt

ALIGNMENTS

conserved hypothetical protein ylxM - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 16-Feb-1944 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A47154; A69882

R;Honda, K.; Nakamura, K.; Nishiguchi, M.; Yamane, K. J. Bacteriol. 175, 4885-4894, 1993

A;Title: Cloning and characterization of a Bacillus subtilis gene encoding a homolog A;Reference number: A47154; MUID:93328695
A;Accession: A47154

A;Status: preliminary

A; Molecule type: nucleic acid A; Residues: 1-110 < HON>

A;Cross-references: GB:D14356; NID:g439700; PIDN:BAA22221.1; PID:g2424968
A;Note: sequence extracted from NCBI backbone (NCBIN:135652, NCBIP:135653)
R;Kunst, F; Ogasawara, N.; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Ber C: Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.; A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D., Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Massuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Seklyuchi, J.; Sekowska, A.; Sea akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, F.; Tognoni, A.; Tosato, V.; Uchlya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A. Reference number: A69580; MUID:98044033

A; Accession: A69882

A;MoLecule type: DNA
A;Residues: 1-110 <KUN>
A;Residues: 1-110 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13470.1; PID:g26339
A;Experimental source: strain 168 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Gene: ylxM C;Superfamily: hypothetical protein A05_orf102

Query Match
Best Local Similarity
6; Conserv Conservative 100.0%; 0; Score 26; Pred. No. Mismatches DB 2; 0; Length 110; Indels

0,

Gaps

0

밁 Ş 69 KLLLLK 1 KLLLLK 6 74

```
C;Accession: C87309

R;Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, R;Lierman, W.C.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                          peptidyl-trNA hydrolase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 14-Sep-2001
C:Accession: C87309
                                                                                                                                                                                   RESULT
C87309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                awa, H.;
DNA Res.
                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: APE1427
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:AP000061; NID:g5104821; A;Experimental source: strain K1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-126 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complete genome sequence of an aerobic A; Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B72621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Kawarabayasi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:AL162756; A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-110 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A81775; MUID:20222556
A;Accession: F81868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Holroyd, S.; Jagels, K.
Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Η.;
                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                         APE1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takamiya, M.; Ma
6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMA1723
                                                                                                                                                                                                                                               KLLLLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLLK
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein APE1427 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y.; Hino, Y.; Horikawa, H.; Yamazaki, ya, M.; Masuda, S.; Funahashi, T.; Tan
                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                  pernix hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aeropyrum pernix (strain
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AL157959; NID:g7380091; PIDN:CAB84951.1; PID:g73803 A, strain Z2491
                                                                                                                                                                                                                                                                                                       Score 26; DE Pred. No. 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DE
Pred. No. 36;
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                     DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyper-thermophilic Crenarchaeon, Aeropy
                                                                                                                                                                                                                                                                                                                                     2:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:BAA80424.1; PID:g5105110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aki, S.;
Tanaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                   Length 126;
                                                                                                                                                                                                                                                                                                                                                                                    APE1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haikawa, Y.; J: T.; Kudoh, Y.;
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jin-no, K.;
.; Yamazaki,
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                           Kolor
C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takal
                                                                                                                                                     A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ.
                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
Nakazaki, N.; Shimpo, S.; Suyımı, ....
Nakazaki, N.; Shimpo, S.; Suyımı, ....
DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing
               A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: C87309
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <STO>
A;Cross-references: GB:AE005673; NID:g13421661; PIDN:AAK22471.1; GSPDB:GN00148
C;GenetLcs:
A;Gene: CC0484
C;Superfamily: peptidyl-trNA hydrolase
                      A;Cross-references: GB:BA000019; PIDN:BAB76941.1; PID:g17134381; GSPDB:GN00179 A;Experimental source: strain PCC 7120
                                                         A; Molecule type: DNA
A; Residues: 1-277 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match.
Best Local Similarity
"""" 6; Conserv
                                                                                        A; Status: preliminary
                                                                                                                                                                                       C;Accession: AB2461
R;Kaneko, T.; Nakamura,
                                                                                                                                                                                                                     A:Note: Anabaena sp. (strain PCC 7120)
C:Date: 14-Dec-2001 #sequence_revision
                                                                                                                                                                                                                                                                         hypothetical protein alr5242 [imported] -
                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                       Species: Anabaena sp.
alr5242
                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                            KLLLLK
                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                               (strain PCC 7120) is a synonym of Nostoc sp. strain PCC sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                       Y.; Wolk,
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                         C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                       Kuritz,
                                                                                                                                                                                                                                                                         Anabaena
                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                     sp.
                                                                                                                                                                                                                                                                                                                                                                                                                       Ö;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 205
                                                                                                                                                                                                                                                                     (strain
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                    Watanabe,
                                                                                                                                                                    Yasuda,
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                     Cyanobacterium
                                                                                                                                                                                                                                    7120
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                    ; Irigu
Tabata
```

```
Matches
                                    Query Match
Best Local
 66
               \vdash
KLLLLK
              KLLLLK 6
                             Similarity 6; Conserv
71
                            100.0%; llarity 100.0%; Conservative 0
                             0;
                                  Score 26;
Pred. No.
                          Pred. No. 86;
Mismatches
                                         2;
                           0;
                                         Length 277
                          Indels
                          0;
                          Gaps
                          0;
```

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat conserved hypothetical protein BBA41 - Lyme disease spirochete plasmid A/1p54 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: A70212 ra, R.; on, M.; Hatch,

₩h

A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic.sequence of a Lyme disease spirochaete,
A;Reference number: A/0100; MUID:98065943 Nature 390, Borrelia burgdorferi

A; Molecule type: DNA A; Status: preliminary; nucleic acid sequence not shown; translation not shown A70212

A; Residues: 1-305 AKLEV

C; Genetics: A; Genome: p A; Cross-references: GB A; Experimental source: GB:AE000790; NID:g2690224; PIDN:AAC66251.1; ce: strain B31 PID: 92690250; TIGR: BB

```
hypothetical protein YLR257w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L8479.9
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999
C;Accession: S51395
R;Miller, N.
                          RESULT
B71482
                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein TC0068 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000 C;Accession: A81745
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
A81745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: The sequence A; Reference number: S51395 A; Accession: S51395
                                                                                   рb
                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                      C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Nucleic Acids Res. 28, 1397-1406, 200. A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November A;Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
hypothetical protein C; Species: Chlamydia
                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002275; GB:AE002160; NID:g7190108; A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-392 <TET>
                                                                                                                                                                                                                                                                                                          A; Accession: A81745
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                          R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-321 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross references: EMBL: U17244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                          Matches
                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: MIPS:YLR257w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 KLLLLK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                              1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK
                                                                                                                                                                                                                                                                                                          preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLLLK 262
                                                                                   KLLLLK 118
                                                                                                                                       6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
                                                                                                                                                                                                             conserved
                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
CT696 - Chl
trachomatis
                                                                                                                                                                                                          hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
             Chlamydia trachomatis
                                                                                                                                                    . 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 0.8;
                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g577171; PIDN:AAB67379.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                    Score 26; DB
Pred. No. 1.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB
Pred. No. 99;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1994
cosmid
                                                                                                                                                                                                                                                                                                                                                                                            S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
                                                                                                                                                                                                          CP0072
                                                                                                                                                                   DB 2;
                                                                                                                                                      2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                            Heidelberg, J.F.; Kolonay, J.; McC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
             (serotype
                                                                                                                                                                                                                                                                                                                                                   MoPn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8479
                                                                                                                                                                Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                PIDN:AAF38951.1; PID:g71901
                                                                                                                                                                                                                                                                                                                                                Chlamydia
             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID: 9577180; GSPDB: GN0001
             strain UW3/Cx)
                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                            McClarty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                          White,
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  pneumoniae
                                                                                                                                                                                                                                                                                                                                                                               ..
...
                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                            ; Hickey,
Salzberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nigg)
                                                                                                                                                                                                                                                                                                                                                   AR39
```

```
망
                             Qy
                                                  Query Match
Best Local Similarity
6; Conserv
                                                                                                                                   A;Gene: CT696
C;Superfamily: conserved hypothetical protein CP0072
                                                                                                                                                                                                                                                                                  A; Title: Genome sequence of an obligate intracellular A; Reference number: A71570; MUID:99000809 A; Accession: B71482
                                                                                                                                                                                                                                                                                                                                     C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000 C;Accession: B71482 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, Science 282, 754-759, 1998
                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                  A;Cross-references: GB:AE001340;
A;Experimental source: serotype 1
                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-403 < ARN>
                                                                                                                                                                                                                                                                    A; Status: preliminary
124 KLLLLK 129
                                 1 KLLLLK 6
                                                                  Conservative
                                                                                100.0%;
                                                                                                                                                                                                     D,
                                                                                                                                                                                                   GB:AE001273; NID:g3329147; PIDN:AAC68291.1;
D, strain UW-3/Cx
                                                                  0
                                                                                  Score 26;
Pred. No.
                                                                  Mismatches
                                                                                  1.2e+02;
                                                                                                   DΒ
                                                                                                Length 403
                                                                                                                                                                                                                                                                                                                     pathogen
                                                                                                                                                                                                                                                                                                                                                      R.; Aravind, L.;
                                                                                                                                                                                                                                                                                                                       of
                                                                  0;
                                                                                                                                                                                                                                                                                                                       humans: Chlamydia
                                                                  Gaps
                                                                                                                                                                                                                   PID:g332
                                                                  0;
                                                                                                                                                                                                                                                                                                                                                        Mitche
                                                                                                                                                                                                                                                                                                                       H
```

RESULT B81910 Query Match Best Local Similarity Thes 6; Conserve A;Gene: NMA1409 C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding A; Residues: 1-542 <PAR>
A; Cross-references: GB: AL162755; A;Reference number: A81775; MUID:20222556 A;Accession: B81910 ; Holroyd, S.; Jagels, K. Nature 404, 502-506, 2000 C; Accession: B81910 R; Parkhill, J.; Acht C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 A; Experimental source: serogroup A; Molecule type: A;Status: preliminary A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491 probable ABC-transporter ATP-binding protein NMA1409 [imported] - Neisseria meningiti Genetics: 10 J.; Achtman, M.; James, S.; Jagels, K.; Leather, DNA Conservative 100.0%; GB:AL157959; NID:g7379742; A, strain Z2491 0, Score 26; Pred. No. K.D.; Bent S.; Moule, Mismatches Bentley, loule, S.; 1.6e+02; DB 2; S.D.; Mungall, Length 542; Indels Churcher, ۳. : PIDN:CAB84649.1; her, C.;; Quail, 0; Gaps cassette Klee, S.R.; Mo Rajandre 0 PID: 9738 homolog

```
Hickey, E.K.; Hart, ....
Hickey, E.K.; Hart, ....
ri, H.; Qin, H.; Vamathevan, J.; v....
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fr.
A;Authors: Complete genome sequence of Neisseria
                                                                                                                                                         R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; II. H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.;
                                                                                                                                                                                                                                ABC transporter, ATP-binding protein NMB1240 [imported] - C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_cC;Accession: E81105
                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                               462 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                    467
                                                                                                                                                                                                                                                            31-Mar-2000 #text_change
                                                                                                                    Fraser, C.M.; Moxon,
                                                                                           meningitidis
                                                                                                                                                                                                                                                                                                        Neisseria meningitidis
                                                                                           serogroup B
                                                                                                                                                                K.E.; Eisen,
Dougherty, B.
Pizza, M.
                                                                                           Rappuoli, R.;
strain MC58.
```

(str

C; Superfamily:

Matches Query Match Best Local :

Similarity 6; Conser

100.

.0%;

Length 542

cassette homology

PID: 972264

Conservative

0;

A;Residues: 1-542 <TET>
A;Cross-references: GB:AE002472; GB:AE002098; NID:g7226475; PIDN:AAF41621.1;
A;Experimental source: serogroup B, strain MC58

unassigned ATP-binding cassette proteins; ATP-binding

```
A; Molecule type: DNA
A; Residues: 1-22 <HER>
R; Braun, A; Barde, Y.A.; Lottspeich, F.; Mewes, W
J. Neurochem. 48, 16-21, 1987
A; Title: N-terminal sequence of pig brain choline
A; Reference number: A28047; MUID:87085562
                                                                                                                           A;Cross-references: GB:03021; NID:9164377; PIDN:AAA31000.1; PID:9164378 R;Hersh, L.B.; Kong, C.F.; Sampson, C.; Mues, G.; Li, Y.P.; Fisher, A.; I. Neurochem. 61, 306-314, 1993 A;Title: Comparison of the promoter region of the human and porcine chol: A;Reference number: PH1571; MUID:93294599 A;Status: translation not shown
A; Molecule type:
                                                                                                                                                                                                                                                                                                   choline O-acetyltransferase (EC 2.3.1.6) precursor - pig C;Species: Sus scrofa domestica (domestic pig) C;Date: 08 -Nov-1991 #sequence_revision 08-Nov-1991 #text_change 05-May-2000 R;Berrard, S.; Brice, A.; Lottspeich, F.; Braun, A.; Barde, Y.A.; Mallet, J. Proc. Natl. Acad. Sci. U.S.A. 84, 9280-9284, 1987 A;Title: cDNA cloning and complete sequence of porcine choline acetyltransferase: A;Accession: A39961; MUID:88097472
                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-641 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RyLawson, D.; Bowman, S.; Barrell, submitted to the EMBL Data Library A, Reference number: 218935
A, Accession: T18437
A, Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C0405c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun C;Accession: T1843-R;Lawson, D.; Bowman, S.; Barrell B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 KLLLLK 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 KLLLLK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C0405c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-608 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: 298547; NID: e1325376; PID: e1325391; PIDN: CAB11116.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrell, B.
Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB
Pred. No. 1.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 2;
Pred. No. 1.6e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                           W.; Thoenen,
                                     acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                              porcine choline acetyltrans:
                                                                                                                                                                                                                  Fisher, A.; Hilt, D.; Baetge
                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                               purified by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                             rapid
                                                                                                                                                                                                                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                 ۲,
```

```
C;Accession: I52631; Average R;Oda, Y: Nakanishi, I: Deguchi, T. R;Oda, Y: Nakanishi, I: Deguchi, T. Brain Res. Mol. Brain Res. 16, 287-294, 19 A;Title: A complementary DNA for human cho recommendation of the complementary DNA for human cho recommendation of the complementary DNA for human cho recommendation of the complementary DNA for human cho
                                                                        C;Species: Homo sapiens (man)
C;Date: 10-Nov-1992 #sequence_revision 13-Mar-1997 #text_change 03-Nov-2000
C;Accession: 152631; A60202; S24416; S14483; PH1571; T01786; PC4342; PC4344;
                                                                                                                                                      N;Alternate names: choline acetylase
                                                                                                                                                                    choline O-acetyltransferase (EC 2.3.1.6) - human
                                                                                                                                                                                                           A60202
                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
""--hes 6; Conserv:
                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Cross-references: EMBL:Z36128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: I
A; Residues: 1-688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49923.1; PID:g296558 R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F. submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S46140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-688 <DOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast 9, 189-199, 1993
A;Title: The complete sequence of a 19,482 bp segment located A;Reference number: S29348; MUID:93220397
A;Accession: S32961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Doignon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Saccharomyces cerevisiae
C; Date: 30-Sep-1993 #Sequence revisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YBR259w - yeast (Saccharomyces N;Alternate names: hypothetical protein YBR1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M27736; NID:g164414; PIDN:AAA31015.1; FC;Comment: This enzyme is responsible for the biosynthesis of C;Superfamily: carnitine O-acetyltransferase C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 2-12 <BRA>
R;Berrard, S.; Brice, A.E.; Mallet, J.
Brain Res. Bull. 22, 147-153, 1989
A;Title: Molecular genetic approach to the study of mammalian choline acetyltransfera A;Reference number: 146574; MUID:89229974
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-641 <BE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993;Accession: S32961; S46140;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                   655 KLLLLK 660
                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                      1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 KLLLLK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae hypothetical protein YBR259w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biteau,
.99, 1993
                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
8 <AIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative 0
                                               I.; Deguchi, T.
Res. 16, 287-294, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.; Crouzet, M.; Aigle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g536684; PIDN:CAA85222.1; PID:g536685; MIPS:YBR2
                                                                                                                                                                                                                                                                                                                                               Score 26; DB
Pred. No. 2e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26;
Pred. No.
                          choline acetyltransferase induces two forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                             DB 2;
2e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2,
1.9e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                Length 688;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g164415
f the neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         right arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                    PC4343
                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0f
                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ac
```

R;Hersh, L.B.; Takane, K.; Gylys, K.; Moomaw, C.; Slaughter, C.

J. Neurochem. 51, 1843-1845, 1988
A;Title: Conservation of amino acid sequences between human and porcine choline acetyltz
A;Reference number: A60202; MUID:89036242
A;Accession: A60202
A;Molecule type: protein
A;Residues: 'XX',163-182;271-295;340-352;376-382;404-415;550-559;572-583;620-632;644-648
A;Residues: 'XX',163-182;271-295;340-352;376-382;404-415;550-559;572-583;620-632;644-648
A;Roussaint, J.L.; Geoffroy, V.; Schmitt, M.; Werner, A.; Garnier, J.M.; Simoni, P.; Kem

```
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 111-119,'T',121-260,'GQ',263-391,'A',393-395,'L',397-433,'G',435-528,'S',A;Cross-references: EMBL:S45018; NID:g257109; PIDN:AAB23557.2; PID:g5705927
R;Misawa, H.; Matsuura, Y.; Oda, Y.; Takahashi, R.; Deguchi, T.
Nol. Brain Res. 44, 323-333, 1997
Nol. Brain Res. 44, 323-333, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 109-150,'Q',152-232 <TOU>
A;Residues: 109-150,'Q',152-232 <TOU>
A;Residues: EMBL:X55685; NID:g29938; PIDN:CAA39923.1; PID:g29939
A;Cervini, R.; Rocchi, M.; DiDonato, S.; Finocchiaro, G.
submitted to the EMBL Data Library, January 1991
A;Description: Isolation and sub-chromosomal localization of a DNA fragmu A;Reference number: S14483
A;Accession: S14483
                                                                                                                                              A;Residues: 119-152 (MIZ)
A;Cross-references: DDBJ:DB2342; NID:g1906789; PIDN:BAA18946.1; PID:d1019687; PID:g19067A;Cross-references: DDBJ:DB2342; NID:g1906789; PIDN:BAA18946.1; PID:d1019687; PID:g19067A;Experimenttal source: brain
C;Comment: This enzyme is responsible for the biosynthesis of the neurotransmitter acetylcholist;C;Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholist;C;Comment: This enzyme is involved in the synthesis of the neurotransmitter acetylcholist;C;Cenetics:
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mkNA
A: Molecule type: mkNA
A: Residues; 119-152 <MI2>
-- man.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: GB:L33837
A;Note: GenBank sequence 9505335 (accession L33837
R;Lorenzi, M.V.; Trinidad, A.C.; Zhang, R.; Straus
DNA Cell Biol. 11, 593-603, 1992
A;Title: Two mRNAs are transcribed from the human
A;Reference number: Z14429; MUID:93000480
A;Accession: T01786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X56879; NID:g29940; PID:g29941
R;Hersh, L.B.; Kong, C.F.; Sampson, C.; Mues, G.; Li, Y.P.; Fisher, A.; Hilt, D.; Baetge J. Neurochem. 61, 306-314, 1993
A;Title: Comparison of the promoter region of the human and porcine choline acetyltrans: A;Reference number: PH1571; MUID:93294599
A;Accession: PH1571
A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: XX',163-182;271-295;340-352;376-382;404-415;550-559;572-583;620-632;644-645 R;Toussaint, J.L.; Geoffroy, V.; Schmitt, M.; Werner, A.; Garnier, J.M.; Simoni, P.; Ken Genomics 12, 412-416, 1992 A;Title: Human choline acetyltransferase (CHAT): partial gene sequence and potential cor A;Reference number: S24416; MUID:92155737 A;Accession: S24416
A;Cross-references: GDB:119775; OMIM:118490
A;Map position: 10q11.2-10q11.2
A;Introns: 129/3; 193/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 119-167, 'E', 169-256
A; Cross-references: DDBJ:D82340
                                                                                                                  A; Gene: GDB: CHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 119-152 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: PC4342; MUID:97225904 A;Accession: PC4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Brain Res. 44, 323-333, 1997
A;Title: Human choline acetyltransferase mRNAs with different 5'-region produce a 69-kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-95 <HE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 688-738 <CER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: PC4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: DDBJ:D82341; NID:g1906787; PIDN:BAA18945.1; PID:d1019686; PID:g1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: PC4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <MI3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <NIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (accession L33837) is Zhang, R.; Strauss, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           missing
7.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a DNA fragment of the huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  choline acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                one nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at
```

```
C;Superfamily: carnitine O-acetyltransferase
C;Keywords: acyltransferase; coenzyme A
```

```
Š
                     Query Match
Best Local Similarity
Matches 6; Conserv
1 KLLLLK 6
                        Conservative
                               100.0%; Score
100.0%; Pred.
                        0;
                         Mismatches
                               No.
                               .2e+02;
                                       Length 748;
                        Indels
                       0;
                       0;
```

В 596 KLLLLK 601

Search completed: June 17, 2002, 12:42:59 Job time: 254 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           욙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq
seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r
      protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
      1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-367-714A-28
26
1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 17, 2002, 12:44:45; Search time 21.35 Seconds (without alignments)
10.881 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105224 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length DB
    38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapext 0.5
IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           066404 aquifex aeo
Q9pln1 chlamydia m
084702 chlamydia t
Pl3222 sus scrofa
    P28329
P07465
P57465
P57465
P25124
P6723866
P6723866
P6723841
P672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P37104 bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                              4 trichoderma
3 saccharomyc
6 mus musculu
7 pseudacanth
9 streptococc
                                                                                                                                                                                                      1 lycopersico
8 homo sapien
8 arabidopsis
5 homo sapien
1 haemophilus
6 haemophilus
6 haemophilus
                                                                                                                                                                                                                                                                                                                                                  7 mycoplasma
5 human herpe
1 helicobacte
1 vaccinia vi
7 homo sapien
1 caldicellul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sus scrofa
saccharomyc
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            semliki f
                                          cyanidium c
actinobacil
                                                                                                                                                                                    oenothera I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermus aqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
YIXM_BACSU STANDARD; PRT; 110 AA.

ID YIXM_BACSU STANDARD; PRT; 110 AA.

AC p37104;
DT 01-OCT-1994 (Rel. 30, Created)
DT 16-OCT-2001 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 13.2 kDa protein in ftsY-ffh intergenic region.
GN YIXM.
OS Bacillus subtilis.
OC Bacillus Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
```

45	44	43	42	41	40	39	38	37	36	35	34
23	23	23	23	23	23	23	23	23	23	23	23
88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5
399	395	394	394	388	362	265	265	208	190	178	156
-	٢	ب	سر	٢	ب	<u> </u>	۲	Н	Н	۲	L
XYLR_ANATH	ARP2_DROME	ARP2_HUMAN	ARP2_CHICK	ARP2_ACACA	MTM1_MICAM	HEM4_MOUSE	HEM4_HUMAN	RL3_HAEIN	YEIP_ECOLI	CASK_RAT	SOXR_PSEAE
Q44406 anaerocellu	P45888 drosophila	015142 homo sapien	P53488 gallus gall		P50190 microbacter	P51163 mus musculu		P44344 haemophilus	P33028 escherichia	P04468 rattus norv	Q51506 pseudomonas

ALIGNMENTS

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                          Q9PLN1;
16-OCT-2001 (
16-OCT-2001 (
16-OCT-2001 (
                                                                                           Gwinn M., Nelson W., DeBoy R.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia
pneumoniae AR39.";
                                                                                                                           Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R. Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=MOPn / Nigg;
MEDLINE=20150255; PubMed=10684935;
                                                                    Nucleic Acids Res.
                                                                                                                                                                                                                                                                   Chlamydia muridarum
                                                                                                                                                                                                                                                                                                                                                                             CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                            Bacteria; Chlamydiales;
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                               Y068_CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasteriand T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hubez Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid ecel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                             KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO A.AEOLICUS AQ_423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE000667; AAC07956.1; -. hetical protein; Plasmid; NCE 194 AA; 23393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquificales;
                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation)
1 protein TC0068.
                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 39,
(Rel. 39,
(Rel. 40,
l protein &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
(Rel.
(Rel.
                                                                    BELONGS
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                  28:1397-1406(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                    TO THE
                                                                                                                                                                                                                                                   Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                              CHLAMYDIAL CPN0675/CT696/TC0068
                                                                                                         trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
816FF102AD5E317D (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
No.
                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                           392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex
                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DВ
23;
                                                                                                         MoPn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                      Chlamydia
                                                                                                                                           Dodson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                               S.L.,
                                                                                                                                                       s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
```

```
RESULT
CLAT_PIG
ID CLAT
AC P132
DT 01-J
DT 01-A
                                                                                                                                                                    Вþ
                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                   Query Match
Best Local s
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SORRECCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 6
  CLAT_PIG
P13222;
01-JAN-1990
01-APR-1990
                                                                                                                                                                    Hypothetical SEQUENCE 3
                                                                                                                                                                                       EMBL; AE001340; AAC68291.2;
                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
MEDIAIN-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fo
Mitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit modified and this sta entities requires a l or send an email to l
                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate chlamydia trachomatis."; Science 282:754-759(1998).
                                                                                                                                                                                                                                                           between
                                                                              113
                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLTR
                                                                                                                                                                                                                                                                                                                                         Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Comp
SEQUENCE 392 AA; 45694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 KLLLLK 118
                                                                                                1 KLLLLK
                                                 ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLLLK
                                                                            KLLLLK
                                                                                                                                                                                                                                                                                        FAMILY.
                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE002274; AAF38951.1; TC0068; -.
                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 100.0%;
Similarity 100.0%;
6; Conservative 0
                                                                                                                                                                   al protein; Complete
392 AA; 45712 MW;
                                                                             118
                                                                                                σ
 (Rel.
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
L protein CT696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
13, Created)
14, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      statement
                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              institutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , WM
                                                                                                                   0,
                                                                                                                 Score 26; DB Pred. No. 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                proteome.
4EC06DEE24CF8E69 CRC64;
                                                                                                                                                                                                                                                                                              CHLAMYDIAL CPN0675/CT696/TC0068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome.
8C7257499347A7C4
                                                                                                                                                                                                                                                                                                                            intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
                             640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              long
                                                                                                                                                                                                                                                                                                                                              Fan J.,
.., Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                             There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
45;
                                                                                                                                     DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                     as its content
                                                                                                                                                                                                                                                                                                                                                         J.,
                                                                                                                                    1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as
                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                             0.,
                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                          pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its content
                                                                                                                                                                                                                                                                                                                                                        Marathe
                                                                                                                                    Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64
                                                                                                                                                                                                                                                                                                                                              rathe R.,
Koonin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                          bу
                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                        a collaboration -
                                                                                                                                                                                                                                                                                                                                               Aravind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is
'for
                                                                                                                 0;
                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                       outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                               Gaps
                                                                                                                                                                                                                          in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercial
                                                                                                                                                                                                                                              on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no
                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

sequence

```
RESULT 6
YB9F_YEAST
ID YB9F_YEAST
                                                                                                                                                                         밁
                                                                                  δÃ
                                                                                                                       Query
Best I
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Néurochem. 48:16-21(1987).

-I. FUNCTION: Catalyzes the reversible synthesis of acetylcholine
-(ACh) from acetyl CoA and choline at cholinergic synapses.
-I. CATALYTIC ACTIVITY: Acetyl-CoA + Choline = CoA + O-acetylcholine.
-I. SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
                                                                                                                                                                                                                    Pfam; PF00755; Carn_acyltransf; 1.
PROSITE; PS00439; ACYLTRANSF_C_1; 1.
PROSITE; PS00440; ACYLTRANSF_C_2; 1.
                                                                                                                                                                                                                                                                     EMBL; J03021; AAA31000.1;
EMBL; M27736; AAA31015.1;
PIR; A28047; A28047.
PIR; A39961; A39961.
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Braun A., Barde Y.-A., Lottspeich "N-terminal sequence of pig brain by a rapid procedure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ventral spinal MEDLINE=89229974; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning and complete sequence of pacetyltransferase: in vitro translation yields an active protein.",
Proc. Natl. Acad. Sci. U.S.A. 84:9280-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ventral spinal MEDLINE-88097472; Publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87085562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berrard S., Brice A., Mallet J.; "Molecular genetic approach to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acetylase)
                                                                                                                                                                                                           Transferase; Acyltransferase;
                                                                                                                                                                                                                                                         InterPro; IPR000542; Carn_acyltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berrard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manumalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last a
Choline O-acetyltransferase
                                                              488
                                                                        1 KLLLLK
                                                                                                                         Local
                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                              KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Res. Bull. 22:147-153(1989)
                                                                                                           6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic approach
sferase.";
                                                                                                                                                                         640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ChAT)
                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brice
                                                              493
                                                                                                            Conservative
                                                                                                                                                                         A,
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
A.
pinal cord;
pinal cord;
2; PubMed=3480542;
3 ce A., Lottspeich F., Braun A., Ba
ce A., Lottspeich F., Braun C., Ba
ce A., Lottspeich F., Braun A., Ba
ce A., Lottspeich F., Braun A., Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=3794697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lnal cord;
PubMed=2713713;
                                                                                                                                                                      333
71599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update) ferase (EC 2.3.1.6) (CHC
                                                                                                                         .0%;
                                                                                                                                   .0%;
                                                                                                                                                                        MW;
                                                                                                            0
                                                                                                                                                                      POTENTIAL.
5ECC27BE8B7CC317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84:9280-9284(1987).
                                                                                                                                                                                                          Neurotransmitter biosynthesis
                                                                                                                         Pred.
  PRT;
                                                                                                                                  Score
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   study
                                                                                                                         No.
                                                                                                                                   26;
  889
                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mewes H.-W.,
                                                                                                                                   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHOACTase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetyltransferase
                                                                                                                                   <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barde Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding
                                                                                                                                                                      CRC64
                                                                                                                                   Length
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thoenen
                                                                                                                                                                                                                                                                                                                                                         γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Choline
                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    choline
                                                                                                                                   640
                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                              EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Η.;
                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mallet
                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                                                                              outstation
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
Ј.,
                                                                                                                                                                                                                                                                                                                                                                       no
                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                           0;
```

```
RRA RRA RRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
CLAT_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 6
                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Spinal cord;
MEDLINE-93180642; PubMed=1337937;
MEDLINE-93180642; PubMed=1337937;
MALANISH I., Deguchi T.;
Oda Y., Nakanishi I., Deguchi T.;
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase"
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase"
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA for human choline acetyltransferase induces two
"A complementary DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30
01-OCT-1994 (Rel. 30
15-JUL-1998 (Rel. 36
Hypothetical 80.4 kD
YBR259W OR YBR1727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1994
01-OCT-1994
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLAT_HUMAN STANDARD: PRT; 748 AA. P28329; Q16488; Q9BQE1; Q9BQ35; Q9BQ23; Q1-DEC-1992 (Rel. 24, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Choline O-acetyltransferase (EC 2.3.1.6) (CHO
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93220397; PubMed=8465606;
Doignon F., Biteau N., Crouzet M., Aigle M.;
"The complete sequence of a 19,482 bp segment located arm of chromosome II from Saccharomyces cerevisiae.";
                                            MEDLINE=21117155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetylase) (ChAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X70529; CAA49923.1;
EMBL; Z36128; CAA85222.1;
PIR; S32961; S32961.
SGD; S0000463; YBR259W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P38338;
                         Ohno K.,
                                                                     AND G-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 9:189-199(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    655 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 100.0%;
Similarity 100.0%;
6; Conservative (
    Tsujino
R., Robb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      688 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
PubMed=11172068;
A., Brengman J.M.,
S., Kirkham F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,
30,
36,
kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
----tein in POP4-SHM1 intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        red. No. 78;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0BA84837BD7A4B30 CRC64;
    Engel
    Harper C.M.,
Engel A.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHOACTase) (Choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetes;
                           Bajzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
Thuman choline acetyltransferase gene.";

RL Neurosci. Lett. 132:191-194(1991).

C. -i- FUNCTION: Catalyzes the reversible synthesis of acetylcholine (Ach) from acetyl CoA and choline at cholinergic synapses.

C. -i- CATALYTIC ACTIVITY: Acetyl-COA+ choline = COA+ O-acetylcholine.

CC -i- ALTERNATIVE PRODUCTS: 3 isoforms; M/83 kDa (shown here), S/74 kDa

CC -i- ALTERNATIVE PRODUCTS: 3 isoforms; M/83 kDa (shown here), S/74 kDa

CC -i- DISEASE: Defects in CHAT are a cause of familial infantile

CC myasthenic gravis type 2 (FIMG2) (also known as CMS-EA). FIMG2

CC myasthenic gravis type 2 (FIMG2) (also known as CMS-EA). FIMG2

CC negative tests for anti-AChR antibodies, and abrupt episodic

CC crises with increased weakness, bulbar paralysis, and apnea

CC -i- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit modified and this st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lymphocytes;
MEDLINE=92149876; PubMed=1784419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervini R., Rocchi M., DiDonato S., Finocchiaro G., Isolation and sub-chromosomal localization of a DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cervini R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 688-738 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Simoni P., Kempf J.;
"Human choline acetyltransferase (CHAT): partial gene sequence and potential control regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 109-232 FROM N.A.
MEDLINE=92155737; PubMed=1339386;
Toussaint J.L., Geoffroy V., Schmitt M., Werner A., Garnier J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acetyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93000480; PubMe
Lorenzi M.V., Trinidad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Two mRNAs are transcribed from acetyltransferase".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 111-669 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Choline acetyltransferase mutations cause myasthenic syndrome associated with episodic apnea in humans.", proc. Natl. Acad. Sci. U.S.A. 98:2017-2022(2001).
                                    AF305907; AAK08953.1;
AF305996; AAK08950.1;
AF305895; AAK08950.1;
AF305895; AAK08950.1;
AF305897; AAK08950.1;
AF305897; AAK08950.1;
AF305897; AAK08950.1;
AF305899; AAK08950.1;
AF305901; AAK08951.1;
AF305895; AAK08951.1;
AF305896; AAK08951.1;
AF305897; AAK08951.1;
AF305897; AAK08951.1;
AF305898; AAK08951.1;
AF305899; AAK08951.1;
AF305901; AAK08951.1;
AF305891; AAK08951.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EMEUROPEAN BIOINFORMATICS INSTITUTE. There are no restrict by non-profit institutions as long as its content of the state 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S56138; AAA14245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d and this statement is not removed. s requires a license agreement (See an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12:412-416(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11:593-603(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1388731;
                                                                                                                                                                                                                                                                                                   0.1;
1. JOINED
1.1 JOINED
                                 JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R., Strauss W.L.;
human gene for choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        уд
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions on
tent is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF305902; AAK08951.1; JOINED EMBL; AF305903; AAK08951.1; JOINED EMBL; AF305904; AAK08951.1; JOINED EMBL; AF305905; AAK08951.1; JOINED EMBL; AF305905; AAK08955.1; JOINED EMBL; AF305909; AAK08952.1; JOINED EMBL; AF305894; AAK08952.1; JOINED EMBL; AF305895; AAK08952.1; JOINED EMBL; AF305896; AAK08952.1; JOINED EMBL; AF305898; AAK08952.1; JOINED EMBL; AF305899; AAK08952.1; JOINED EMBL; AF305899; AAK08952.1; JOINED EMBL; AF305900; AAK08952.1; JOINED EMBL; AF305901; AAK08952.1; JOINED EMBL; AF305902; AAK08952.1; JOINED EMBL; AF305902; AAK08952.1; JOINED EMBL; AF305903; AAK08952.1; JOINED EMBL; AF305904; AAK08952.1; JOINED EMBL; AF305904; AAK08952.1; JOINED EMBL; AF305904; AAK08952.1; JOINED EMBL; AF305905; AAK08952.1; JOINED EMBL; AF305906; 
                                                                                                              VARSPLIC
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000542; Carn_acyltransf.
Pfam; PF00755; Carn_acyltransf; 1.
PROSITE; PS00439; ACYLTRANSF_C_1; 1.
PROSITE; PS00440; ACYLTRANSF_C_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                        1
151
261
396
434
529
567
629
664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Disease
442 442 F
120 120 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392
                                                                                                           AA;
                                                                                             118
151
262
396
434
529
567
630
664
82567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210
0.0%;
                                                                                                              / FTIG-VAR, 011674.
/FTIG-VAR, 011674.
/FTIG-VAR, 011674.
MGLRTAKKRGLGGGKWKREEGGGTRGRREVRPACFLQSGG
RGDPGDVGGPAGNPGCSPHPRAATRPPLAHTPEWC
GAASAERAEPRA -> MWPECRDEALSTV (IN
ISOFORM S).
MISSING (IN ISOFORM R).
R -> Q (IN REF. 4).
GQ -> PE (IN REF. 1).
V -> L (IN REF. 3).
C -> S (IN REF. 3).
C -> S (IN REF. 3).
V -> L (IN REF. 3).
V -> L (IN REF. 3).
L (IN REF. 3).
V -> L (IN REF. 3).
V -> L (IN REF. 3).
                                                                                                           W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L -> P (IN FIMG2;
/FTId=VAR_011666,
P -> A (IN FIME2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V -> L (IN FIMG2;
/FTId=VAR_011673.
R -> H (IN FIMG2;
/FTId=VAR_011674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_011670.
R -> G (IN FIMG2;
/FTId=VAR_011671.
S -> L (IN FIMG2;
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_011672;
V -> r. /rw --
                                                                                                L -> DV (IN REF. 3)
-> M (IN REF. 3)
0D537659F876C497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_011676.
R -> C (IN FIMG2;
/FTId=VAR_011669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P -> A (IN FIMG2;
/FTId=VAR_011667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I -> T (IN FIMG2; /FTId=VAR_011668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_011675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurotransmitter biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
G
```

entities or send a

(IN FIMG2;

COMPLETELY LACK IMPAIRED ACTIVITY).

IMPAIRED IMPAIRED

ACTIVITY) ACTIVITY). IMPAIRED ACTIVITY).

IMPAIRED ACTIVITY). IMPAIRED ACTIVITY). IMPAIRED ACTIVITY). the

This between

EMBL, EMBL,

EMBL; EMBL; EMBL;

26; No.

DB 85;

Length 748;

```
POLICE PO
      H H A H
                                                                                        RESULT: 9
                                                                                                                                                                                                                   Q
                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
  Y385_BUCAI
P57465;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLN_SFV
P08411;
01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V.IS_
                                                                                                                                                                             1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polyprotein;
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002589; Alpp.
InterPro; IPR002620; Peptidase_C9.
InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR000606; Viral_helicase1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long amodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids Res. 14:5667-5682(1986).
-I- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION
-I- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=86286581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; C09.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entitles requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Semliki Forest virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSP4
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A23592; MNWVSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Semliki forest virus (SFV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           596
                                                                                                                                                                                                     1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                             KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00978; RNA_dep_RNApol2; PF01443; Viral_helicase1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF01661; Alpp; 1.
PF01707; Peptidase_C9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X04129; CAA27741.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00506; Alpp;
                                                                                                                                                                                                                                                           h 100.0%;
Similarity 100.0%;
6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                   \begin{array}{c} 1818 \\ 2431 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                             1868
(Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nonstructural
1 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positive-strand viruses,
                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     A
A
                                                                                                                                                                                                                                                                                                                                                                                       2431
                                                                                                                                                                                                                                                                                                                                                                                                           1335
1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=3488539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of the nonstructural
                                                                                                                                                                                                                                                                                                                                                               ctural protein; RNA-binding; Helicase.
37 NONSTRUCTURAL PROTEIN NSP1.
35 NONSTRUCTURAL PROTEIN NSP2.
17 NONSTRUCTURAL PROTEIN NSP3.
31 NONSTRUCTURAL PROTEIN NSP4.
269286 MW; 1F9EBA1022E3EC5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [Contains:
                                                                                                                                                                                                                                                             00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                        Score 26; DB 1;
Pred. No. 2.7e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural
                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no DNA stage; Togaviridae;
                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                Length 2431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
tent is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSP1 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER REPORT OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         STRAIN-ATCC 33923 / AT-62;
MEDLINE-91238680; PubMed=2034208;
MISHAYAMA M., Horinouchi S., Beppu T.;
"Characterization of an operon encoding succinyl-CoA synthetase and malate dehydrogenase from Thermus flavus AT-62 and its expression in Escherichia coli.";
Mol. Gen. Genet. 226:1-9(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus aquaticus (subsp. flav
Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002634; BolA.

Pfam; PF01722; BolA; I.

Hypothetical protein; Complete proteome.

SEQUENCE 80 AA; 9299 MW; 4AFACA590A038131 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20445173; PubMed=10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           symbiotic bacterium).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Hypothetical protein BU385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSC1_THEFL P25124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE YCF81 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001119; BAB13088.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 407:81-86(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-TOKYO 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLLLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 40, Last annotation update)
protein in SCSB 5'region (ORFA) (Fragment).
+ious (subsp. flavus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELONGS TO THE BOLA / YRBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Last annotation update) BU385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group; Thermus group; Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.;
aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO E.COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

EMBL; X54073; CAA38004.1;

```
RESULT
Y245_WI
ID 27
ID 
                                         ID
AC
DT
                                                                                           UL24_HSV7J
                                                                                                              RESULT
                                                                                                                                                                      Дb
                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                       Query
Best I
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΩV
                                 UL24_HSV7J
P52386;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR
DR
FT
SQ
                                                                                                                                                                                                                                                                                                   InterPro; IrR002698; 5-FTHF_Cyc-lig.
Pfam; PF01812; 5-FTHF_Cyc-lig; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 165 AA; 19355 MW; AEC4ADEEE55A7020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL. The European Bioinformatics Institute. There are no restrict modified and this statement is not removed. Usage by and foor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed=7569993;

Fraser C.M. Gocayne J.D. White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucter T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U39703; AAC71465.1;
                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MG245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYCGE
Y245_MYCGE
P47487;
01-0CT-1996
01-0CT-1996
16-0CT-2001
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
Hypothetical protein MG245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                  9
                                                                                                                                                                                1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S15948; S15948.
InterPro; IPR002792;
Pfam; PF01938; TRAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                                            KLMLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 KLLILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                   Similarity 5; Conserv
                         (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 5; Conserv
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 34, Created)
(Rel. 34, Last seg
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA; 10011 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                             92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUF90
                                                                                                                                                                                                                                                                                                                                                                                                              ŀ
                                                                                                                                                                                                                   ; Score 24; DB; Pred. No. 59; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC3B333389B9CCCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                         239
                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165
                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                   Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 93;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and for
                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its
                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
```

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD R RD CCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                      MEDLINE-93139035, PubMed-7678592;
Evans D.G., Karjalainen T.K., Evans D.J., Graham ["Cloning, nucleotide sequence, and expression of a adhesin subunit protein of Helicobacter pylori.",
J. Bacteriol. 175:674-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 13
1_HELPY
HPA1_HELPY
Q48264;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                 -!- PTM: THE N-TERMINUS IS
                                                                                                                                                                                                                                                                                                                            Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Neuraminyllactose-binding hemagglutinin precursor (N-acetylneuraminyllactose-binding fibrillar hemagglutinin receptor-
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                  binding subunit) (NLBH) (FlageIlar sheath adhesin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@fisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (
16-OCT-2001 (
Protein U49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV
EHV-1 37, EBV BXRF1, HCMV UL/6, ILTV ORF3, AND VZV 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpesvirus (type 7 / strain JI) Viruses; dsDNA viruses, no RNA stage; Alphaharpesvirinae; Simplexvirus. NCBL_TaxID=57278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Nicholas J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 KILLLK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR002580; Herpes_UL24.
PF01646; Herpes_UL24; 1
NCE 239 AA; 28568 MW; F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U43400; AAC54711.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34, Last sequence update; 40, Last annotation update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.3%;
                                                                                                                                 BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB Pred. No. 85;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F4EBC038679BE6B0 CRC64;
                                                                                                                                                      to the outer membrane
        (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HHV7).
                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239;
                                                                                                                                                                                                       a D
                                                                                                                                                                                                     .Y., I
                             γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                     Ьее
                                                                                                                                                                                                  encoding
                                                                                                                                                        bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSV-1 UL24,
                                                                                                                                                                                                                     ი.
                           for
                                                                                                                                                    a lipid
     .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                   an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
```

Ċ

```
RESULT
VC17_VA
   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR ETT FTT SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-FEB-1991 (Rel.: 01-FEB-1991 (Rel.: 1 16-OCT-2001 (Rel.: 4 Protein C17/B23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VC17_VACCC
P21101;
01-FEB-1991
                                                                                                                                           PROSITE;
                                                                                                                                                                         InterPro; IPR002110; ANK. Pfam; PF00023; ank; 3. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the property of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Appendix to 'The complete DNA Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goebel S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goebel S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinia virus (strain viruses, dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
     SEQUENCE
                                                                                                                                                                                                                                                              EMBL; M35027; AAA48222.1; -. EMBL; M35027; AAA47979.1; -.
                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B23R AND C17L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flagella;
                     REPEAT
                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete DNA sequence Virology 179:247-266(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoletti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ب
                                                                                                                                                                                                                              D42528;
F42502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILLLK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X61574; CAA43773.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conser
                                                                                                                                         PS50088; ANK_REPEAT; FAL
PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                              : D42528.
: F42502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
28
28
134
                                                                                                                         Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson G.P., Perkus
     ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17,
17,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
260
28
139
                   91
126
245
280
321
381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29166
   44941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copenhagen).
, no RNA stage; Poxviridae; Chordopoxvirinae;
   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein; Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perkus
ANK 1.
ANK 2.
ANK 3.
ANK 4.
ANK 5.
ANK 5.
ANK 5.
ANK 6.
ANK 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ.
N-ACYL DIGLYCERIDE (PROBABLE).
N-ACETYL-NEURAMINYL-ALPHA (2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).
; 22489598065E7B14 CRC64;
                                                                                                                                                       FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ε.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .E., Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.
ı; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рв
93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of vaccinia virus'.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲.
                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Winslow J.P.,
                                                                                                                                                                                                                                                                                                                                                   bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Winslow
                                                                                                                                                                                                                                                                                                                                                   and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                   n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
```

```
Qy
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNM2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
DNA (cytosine-5)-methyltransferase-like protein 2 (DN
DNA (cytosine-5)-methyltransferase homolog HsaIIP) (DNA MTase homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   014717;
                                        EMBL; AF012128; AAC51939.1; -.
EMBL; AJ223333; CAA11272.1; -.
EMBL; AL133415; CAB87964.1; -.
PDB; 1G55; 17-JAN-01.
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                Dong A., Yoder J.A., Zhang X., Zhou L., Bestor T.H., Cheng X.; "Structure of human DNMT2, an enigmatic DNA methyltransferase that displays denaturant-resistant binding to DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98258972; PubMed-95990
Van den Wyngaert I., Sprengel
"Cloning and analysis of a nov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98087580; PubMed=9425235; Yoder J.A., Bestor T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNM2_HUMAN
                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                           entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 29:439-448(2001).
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20580737; PubMed=11139614;
                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 426:283-289(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fission yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A candidate mammalian DNA methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (M.HsaIIP) (PuMet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 KLLLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLLLK 6
                                                                                                                                                                                                                               TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                           recognizing motif.
TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                      FUNCTION: Seems not be active as a DNA methyltransferase. strong binding to DNA suggests that it may mark specific in the genome by binding to DNA through the specific targ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:279-284(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9599025;
I., Sprengel J., Kass
ysis of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ယ္
မေ
မေ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB
Pred. No. 1.4e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 1.4e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.U., Luy
putative
                                                                                                                                                        There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luyten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related
                                                                                                                                                                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 386,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DNA
                                                                                                                                            bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSaIIP)
                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pmt1p
                                                                                                                                                                                                                                                                           target-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                              for
                                                                                                                                                                                                                                                                                         sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
f
                                                                                                                              .ch/announce/
                                                                                                                                                                                                                                                                                                                                                 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                           way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

REBASE; 3241; M.HsaIIP. MIM; 602478; -.

IPR001525; C5_DNA_meth

```
DR Pfam; PF00145; DNA_methylase; 2.
DR PRINTS; PR00105; CS_MTARSE_1; FALSE_NEG.
DR PROSITE; PS00094; CS_MTASE_2; 1.
RR PROSITE; PS00095; CS_MTASE_2; 1.
RW DNA-binding; 3D-structure. BY SIMILARITY.
SQ SEQUENCE 391 AA; 44596 MW; BCA549E4EB2E6950 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 391;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QV 1 KLLLLK 6
Db 334 KLLLLK 339

Search completed: June 17, 2002, 12:44:46

Search completed: June 17, 2002, 12:44:46
```

```
Title:
Perfect score:
                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     No
                                                                                                                                                                                                                                      Pred: No.
score grea
and is der
                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq
                                                                                                                                                                                                                                                 greater
                                                                                                                                266
                                                                                                                                                                                                                                        derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length:
                                                                                                                               100.0
100.0
100.0
                                                                                                                                                                                     Match
                                                                                                                                                                                                                                      is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
    June 17, 2002, 12:44:18; Search time 73.61 Seconds (without alignments)
14.101 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-367-714A-28
26
1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                  sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                            sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                       sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                      sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                               sp_fungi:*
                                                                                                                                                                                                                                                                                          sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                              sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                            invertebrate:*
                                                                                                                                                                                                                                                                                                                                    sp_virus:*
                                                                                                                                                                                                                                                                                                                                             sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                       sp_plant:*
                                                                                                                                                                                     Length
    DB
                                                       16
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapext 0.5
                                                                                                 16
                                                                                                                     16
   Q9G8N5
Q9JZ89
Q9JUB3
Q9HGZ7
Q93N56
Q9TWB0
Q95TP6
Q77331
                                                                                                                              Q9YC24
Q9P7A2
                                                                                                          Q9MG96
                                                                                                                                                              Q95T00
                                                                                      Q06146
                                                                                                                                                                                     Ħ
                                                                                                 050934
                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562222
Q95t00 drosophila
Q9jt16 neisseria m
Q9yc24 aeropyrum p
Q9yc24 aeropyrum p
Q9p7a2 schizosacch
Q9aav9 caulobacter
Q9mg96 chrysodidym
O50934 borrelia bu
Q06146 saccharomyc
Q9g8n5 naegleria g
Q9js89 neisseria m
Q9jub3 neisseria m
Q9jub3 neisseria bu
Q9twb0 plasmodium
Q95tp6 drosophila
Q77331 plasmodium
                                                                                                                                                                                  Description
```

.ω	92	92.3	·w	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	92.3	100	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100	100.0	26 100.0 614
16 Q9PMD0	16 Q98EW8	8 Q9MTD5	16 Q9ZLJ3	16 025359	_	o	16 Q9PKE1			_	Ö				_		0		_		O			o		O		12 041268
Q9pmd0 campylobact	Q98ew8 rhizobium l	Q9mtd5 toxoplasma	Q9zlj3 helicobacte	025359 helicobacte	Q9rnc3 helicobacte	7	Q9pke1 chlamydia m	O84255 chlamydia t	Q92anl listeria in	Q96sl4 homo sapien	Q9rnc2 helicobacte	Q9jr77 neisseria m	Q9xek3 dendrobium	Q930x5 rhizobium m	Q35715 romanomermi	Q91g10 oryza sativ		Q9qbml semliki for				024367 spirodela p	Q99mz9 mus musculu	Q9ngx1 entamoeba h	Q83611 ectromelia	Д	Q91mw5 lumpy skin	O41268 semliki for

ALIGNMENTS

```
RESULT 2
Q9JTL6
ID Q9JTL6
                                                                                                                  Query Match
Best Local Similarity
Thehes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q95T00
                                                                                                                                                                                                       밁
                                                                                                  Q
                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacles J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY06401; AAL254401; -.
EMBL; AY06401; AAL254401; -.

SEQUENCE 58 AA; 7029 MW; 4CE54127CB70AA98 CRC64;
                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARYBDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q95T00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95T00;
                                                                         53
                                                                                         1 KLLLLK 6
                                                                         KLLLLK
                                                                         58
   PRELIMINARY;
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                0;
                                                                                                                                             Score 26;
Pred. No.
   PRT;
                                                                                                                                Mismatches
   110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
                                                                                                                                0;
                                                                                                                                                            Length 58;
                                                                                                                                Indels
                                                                                                                                0;
                                                                                                                                Gaps
                                                                                                                                0;
```

밁

62

67

```
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                       Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug Hosoyama A., Fukui S., Nagal Y., Nishijima K., Nakazawa H., Takaniya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999
01-NOV-1999
01-MAR-2001
                                                                                  Hypothetical protein; Complete SEQUENCE 126 AA; 14192 MW;
                                                                                                                       Crenarchaeon, Aeropyrum pernix DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;

MEDLINE=2022256; PubMed=10761919;

Parkhill J. Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria

meningitidis 22491.";

Nature 404:502-506(2000).

EMBL; AL162756; CAB84951.1; -.
                                                                                                                                                                                                                                  MEDLINE=99310339;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                       Q9YC24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09JTL6;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                      Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                      Aeropyrum
                                                                                                                                                                                                                                                                                                                                 APE1427
                                                                                                                                                                                                                                                                                                                                                                                             Q9YC24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMA1723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUTATIVE PROLINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK
 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLLLLK
                                                                                                        AP000061; BAA80424.1; -.
                       Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteome.
                                                                                                                                                                                                                                                                                                                    pernix.
6
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA;
                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last seque
(TrEMBLrel. 16, Last annot
L 14.2 KDA PROTEIN APE1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                 PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12714 MW;
                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                     Desulfurococcales;
                     0;
                                                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                   Score 26; DE
Pred. No. 68;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB Pred. No. 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN.
                                                                             proteome.
B766FEF18B135029 CRC64;
                                                                                                                                K1.";
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F8ED83151FC34CB8
                                                                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
61;
                                             DВ
                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                    Desulfurococcaceae;
                                           17;
                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                           Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                      Kosugi H.,
                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

```
RESULT QPAAV9

IDAAV9

IDAAV9

AC Q9

DT 011

DT 011

DT 011

DT 011

DT 011

CC Ca

C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                              EQUENCE FROM N.A.

C STRAIN-ATCC 19089 / CB15;

X MEDILINE-21173698; PubMed-11259647;

X MEDILINE-21173698; PubMed-11259647;

X Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K. A. Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., A. Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry A. Utterback T., Trant K., Wolf A. W., Vamathevan J., Ermolaeva M., Whi Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

A. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRALIF...

MCCombie W.R.;

Submitted (APR-1999) to the EN
EMBL; ALI63702; CAB87363.1; -

EMBL; ALI63702; TAB87363.1; -

EMBL; ALI64702; TAB87363.1; -

EMB
InterPro; IPR001328; Pept_trNA_hydro.
Pfam; PF01195; Pept_trNA_hydro; 1.
ProDom; PD005324; Pept_trNA_hydro; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AAV9;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                   EMBL; AE005721; AAK22471.1; HSSP; P23932; 2PTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000
01-0CT-2000
CYTOPLASMIC
                                                                                                                      TIGR; CC0484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDYL-TRNA HYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AAV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972H-;
Seeger K., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPBP35G2.01C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9P7A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9P7A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
nilarity 100.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TremBLrel. 15, Created)
(TremBLrel. 15, Last sequence update)
(TremBLrel. 15, Last annotation updat
(TremBLrel. 15, Last annotation updat)
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood V., Rajandream M.A., Barrell B.G.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17,
17,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Created)
, Last sequence up
, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB Pred. No. 78; D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5D283F44B9426B13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                 N.D., Ely
                                                                                                                                                                                                                                                                                                                                             Berry K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     ₿.,
```

0

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9MG96;
01-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
 SEQUENCE FROM N.A. STRAIN=ATCC 35210 / MEDLINE=98065943; p Fraser C.M., Casjen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLING-20330374; PubMed-10871400;
                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Creat 01-JUN-1998 (TrEMBLrel. 06, Last 01-NOV-1998 (TrEMBLrel. 08, Last CONSERVED HYPOTHETICAL PROTEIN.
                                                                 Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                Plasmid lp54.
Bacteria; Spi
                                                                                                                                                                                                     050934
                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion.
SEQUENCE 265
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synuroideus. Complete
organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9MG96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
SEQUENCE
                                                                                                        Borrelia burgdorferi
                                                                                                                         BBA41
                                                                                                                                                                                       050934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chrysodidymus synuroideus
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=47573;
                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                          KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLLLK
                                                                                                                                                                                                                                                                       KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                              tted (JAN-2000) to the EMBL/G
AF222718; AAF36953.1; -.
Pro; IPR001351; Ribosomal_S3.
                                                                                                                                                                                                                                                                                                                                                                                                                    PF00189;
Ç
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete 205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stramenopiles;
                                                                                                                                                                                                                                                                       104
                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
 Casjens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res.
                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal_S3_C;
               / B31;
PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28:2512-2518(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteome.
22472 MW;
                                                                                                                                                                                                                                                                                                                                                                                          31348
                                                                                                                                                                                                                                                                                                                                     100.0%;
  s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
                                                                                                        (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 08;
Huang
                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chrysophyceae;
                                                                                Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
                                                                                                         disease
                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                      Score 26; DB Pred. No. 1.3); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB
Pred. No. 1.1
); Mismatches
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 Σ.
Χ.
                                                                                                                                                                                                                                                                                                                                                                                          D985AB230A78220E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F64F92A527D6B8F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                               sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stramenopile
                                                                                                        spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ocampo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        content
 Sutton
                                                                                                                                                                                                    305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265
                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ċ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synurales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                     .3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1e+02;
                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                               update)
 G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lang
                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alga Chrysodidymus
                                                                                                                                                                                                                                                                                                                                                Length 265;
                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
 Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chrysodidymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205;
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
ALD DATE OF SERVICE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
```

```
RESULT
Q06146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weldman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., H. Smith H.O., Venter J.C.;
                                                                                   STRAIN=S288C (AB972);
Cherry J.M.;
Submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Kotter P., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P., Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D., Muller-Auer S., Nentwich U., Obermaler B., Piravandi E., Pohl Muller-Auer S., Nentwich U., Obermaler B., Rieger M., Rinke M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., "The nucleotide sequence of Saccharomyces cerevisiae chromosomus and the second sequence of Saccharomyces cerevisiae chromosomus and the second sequence of Saccharomyces cerevisiae chromosomus and the second sequence of Saccharomyces cerevisiae chromosomus and the sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
MEDLINE-97313267; PubMed-9169871;
Johnston M., Hillier L., Riles L.,
Johnston M., Hillier L., Riles L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TIEMBLIEL 01, 01-NOV-1996 (TIEMBLIEL 01, 01-JUN-2001 (TIEMBLIEL 17, CHROMOSOME XII COSMID 8479. YLR257W OR L8479.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               burgdorferi.";
Nature 390:580-586(1997)
EMBL; AE000790; AAC66251
Submitted (AUG-1997) to tl
EMBL; U17244; AAB67379.1;
SGD; S0004247; YLR257W.
SEQUENCE 321 AA; 35998
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                    Waterston
                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                   Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q06146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q06146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KILLLK
| | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BBA41;
                                                                                                                                                                                                                                                                                                                                                                   z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 100.0%;
Similarity 100.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete 305 AA;
                                                                                                                                                                                                                                    æ
:
                                                                                                                                                                                                          (NOV-1994)
                                                                                                                                                                                                                                                                                                                                     (NOV-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC66251.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome
1; 34953 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetaceae;
  35998
                                                                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a Lyme disease
                                                                           the
                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
  MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , WM
                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.,
  E8E1FC17FFB27418 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8A57A4FDF9972F9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K., Andre E
Dusterhoft
                                                                              databases
                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoheisel J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andre B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ansorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gwinn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

```
RESULT
Q9JZ89
ID Q9
AC Q9
DT Q1
RON NI
COC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT

OGGRAS

AC QS

DT QS

N QS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
SEQUENCE FROM N.A.

STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Nelson T., Ciecko A., Marche O., Fleischmann R.D., Dougherty B.A.
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JZ89;
Q9JZ89;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC TRANSPORTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9GBN5 PRELIMINARY;
Q9GBN5;
Q1-MAR-2001 (TrEMBLrel. l.
Q1-MAR-2001 (TrEMBLrel. l.
Q1-JUN-2001 (TrEMBLrel. l.
RIBOSOMAL PROTEIN S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The mitochondrial genome of the supposedly primitive protist, Naegleria gruberl.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288092; AAG17819.1;
InterPro; IPR002942; S4.
Ffam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naegleria gruberi.
Mitochondrion.
Eukaryota; Heterolobosea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 KLLLLK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) (Tremblrel. 15, C)
) (Tremblrel. 15, L;
l (Tremblrel. 19, L;
l Tremblrel. 19, L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16,
16,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizopyrenida; Vahlkampfiidae; Naegleria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DE
Pred. No. 1.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0A7A5A9E1AB58EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĀΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                     Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                               B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

DЬ γQ

```
RESULT
Q9HGZ7
ID Q9:
AC Q9:
DT 01
DT 01
DT 01
DE CY
                                                                                                                                    В
                                                                                                                                                        Qy
                                                                                                                                                                                Matches
                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR DR DR DR DR DR DR DR DR SQ
       01-MAR-2001
01-MAR-2001
01-DEC-2001
CYTOPLASMIC I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
                                                          Q9HGZ7
Q9HGZ7;
                                                                                                                                                                                                                                  Pfam; PF00005; ABC_tran; 2.
SMART; SM00382; AAA; 1.
ATP-binding; Complete proteome.
SEQUENCE 542 AA; 60723 MW;
                                                                                                                                                                                                                                                                              Nature 404:502-506(2000).
EMBL; AL162755; CAB84649 1;
InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003439; ARC_transportr.
                                                                                                                                                                                                                                                                                                                                            Parkhill J., Achtman M., James K.D., Bentley S.D., Chur Klee S.R., Morelli G., Basham D., Brown D., Chillingwor Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N. Rajandream M.A., Rutherford K.M., Simmonds M., Skelton Whitehead S., Spratt B.G., Barrell B.G., Skelton "Complete DNA sequence of a serogroup A strain of Neiss meningitidis Z2491."
                                                                                                                                462 KLLLLK
                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003593; Amn.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IRR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 2.
SMART; SM00382; AAA; 1.
ATP-binding; Complete proteome.
SEQUENCE 542 AA; 60778 MW; 1EACB1DC50077CE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Z2491 / SEROGROUP A / SEROTYPE MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Z2491 / SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ABC-TRANSPORTER ATP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JUB3;
01-ОСТ-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09ливз
                                                                                                                                                     1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:1809-1815(2000).
EMBL; AE002472; AAF41621.1;
TIGR; NMB1240; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 KLLLLK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLLK 6
                                                                                                                                                                              6;
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
(TrembLrel. 16, Created)
(TrembLrel. 16, Last sequence update)
(TrembLrel. 19, Last annotation update)
DYNEIN INTERMEDIATE CHAIN.
                                                                                                                                467
                                                                  PRELIMINARY;
                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                          0;
                                                                                                                                                                      Score 26; DB
Pred. No. 2.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                               715362DFF1AB7527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                K.D., Bentley S.D., Churcher C.,
D., Brown D., Chillingworth T.,
D., Hamiln N., Holroyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; [Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                              544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 AA
                                                                                                                                                                                                DB 16;
                                                                                                                                                                      .6e+02;
s 0;
             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6e+02;
s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                       of Neisseria
                                                                                                                                                                                            Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     s.
                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

SPBC855.01C. Schizosaccharomyces

3

```
RESULT
1093N56.
1D 2093N56.
1D 2093N56.
RESULT
Q9TWB0
                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                     Query Match
Best Local s
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. HOOVER T.A., VOOKIN M.H., Williams J.C., Culp "A chromosomal DMA deletion explains the pheno burnetii phase II variant.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; AF387640; AAK71266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE: PS50082; WD_REPEATS_2; 1.
PROSITE: PS50294; WD_REPEATS_REGION; 1.
Repeat; WD_repeat
Repeat; WD_repeat
SEQUENCE 544 AA; 60960 MW; 1057A3C5435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 62.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 5. SMART; SM00320; WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ c-i- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP EMBL; AL391016; CAC01482.1; -.
                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSHL Advanced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxiella group;
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Coxiella group; Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q93N56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q93N56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCombie W.R., Lyne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               course.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972H-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence of a
                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                           ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                μ
                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLLLLK
                                                                                                            KLLLLK
                                                                                   KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLLLK
                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 6; Conser
                                                                                                                                                                                                                                                                             of protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.
Conservative
                                                                                      371
                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.9
                                                                                                                                                                                                                                                                           ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                           62831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ťo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cosmid insert determined during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 09;
                                                                                                                                                                                                                                                                           WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subdivision; Legionellaceae
                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                 Score 26; DB Pred. No. 2.6); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DE Pred. No. 2.6); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                           FACC03057E3CE23B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1057A3C5435F3E6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547
                                                                                                                                                                   2.6e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                              Culp D.W., phenotype (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DΒ
                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                         databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                                                         Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 544;
                                                                                                                                                                                                                                                                                                                                                                              of the Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two
                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 week
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                   0;
```

```
RESULT 095TPG 1D 7Q9 DT 00 DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A CONTRACTOR OF THE CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C -!- MISCELLANGUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERAS C ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSI C DIFFERENT REACTIONS OF DNA SYNTHESIS (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

R InterPro; IPRO02094; DNA,POL_B.

R Pfam; pF00136; DNA,POL_B; 1.

R Pfam; pF00136; DNA,POL_B.

R Pfam; pF00136; DNA,POL_B.

R PFAMT; SM00486; POLDE; 1.

R PRINTS; PR00106; DNAPOLB.

R PROSITE; PS00116; DNA,POLB.

R PROSITE; PS00116; DNA,POLB.

R PROSITE; PS00116; DNA,POLB.

DNA TEPLICATION; DNA-DINGHASE, UNKNOWN_1.

R PROSITE; PS00136; SUBTILASE, ASP; UNKNOWN_1.

DNA TEPLICATION; DNA-DINGHASE, DNA-GIRECTED DNA POLYMERASE.

DNA TEPLICATION; DNA-DINGHASE, SABRETZ7561358D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q95TP6;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9TWB0;
01-MAY-2000
01-MAY-2000
01-DEC-2001
SEQUENCE FROM N.A.

STRAIN-Y, CN BW SP;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall

Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S.,

Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY058628; AAL13857.1;

EMBL; AY058628; AAL13857.1;

SEQUENCE 576 AA; 63439 MW; 0588C7F8E07E1249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q95TP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINB=92107655; PubMed=1762904;
Ridley R.G., White J.H., McAleese S.M., Goman M., Alano P.,
de Vries E., Kilbey B.J.;
"DNA polymerase delta: gene sequences from Plasmodium falciparum
indicate that this enzyme is more highly conserved than DNA polym
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthrop
Pterygota; Neoptera; Endopt
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LD32549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 19:6731-6736(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA POLYMERASE ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 KLLLLK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE PYROPHOSPHATE + DNA(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Diptera; Brachycera; Muschilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13, Createu,
13, Last sequence up
19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RE FIVE DNA POLYMERASES:

NWHICH ARE RESPONSIBLE
(BY SIMILARITY).

TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 560
                                                                                                                                                                                                  George
ngall C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muscomorpha;
                                                                                                                                                                Wan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase
                                                                                                                                                                                              ū,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR
```

0

Query Match Best Local Similarity

100

.0%;

Score Pred.

No.

DB 5; 2.7e+02;

Length

	Sear Job	DЬ	Qy	M
	ch co	347		Matches
	Search completed: Job time: 295 sec	347 KLLLLK 352	1 KLLLLK 6	
	ec d:	×-	- 5	0
	Search completed: June 17, 2002, 12:44:20 Job time: 295 sec	52		6; Conservative
	, 2002			tive
	, 12			0;
	: 44			×
•	:20			0; Mismatches
				0;
			•	0; Indels
				0;
				0; Gaps
				0;

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein + protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*

1: /cgn2_6/ptodata/2,

2: /ggn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /ggn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                     100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 17, 2002, 12:42:03; Search time 34.71 Seconds (without alignments) 4.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-367-714A-28
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length DB
                       2431
187
187
401
401
564
565
905
1066
11226
11226
11226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapext 0.5
S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compugen Ltd
                                      sequence
                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                         10,
Appli
```

22 84.6 9 2 US-08-621-259A-215 22 84.6 9 2 US-08-621-259A-215 22 84.6 9 4 US-09-217-352-219 22 84.6 9 4 US-09-217-352-219 22 84.6 46 2 US-08-312-202B-2 28 84.6 46 3 US-09-079-347-2 22 84.6 46 3 US-09-079-347-2 22 84.6 46 3 US-09-173-151A-12 22 84.6 100 4 US-09-173-151A-6 22 84.6 120 4 US-09-173-151A-6 22 84.6 309 1 US-08-213-151A-6 22 84.6 309 1 US-08-213-151A-6 22 84.6 309 4 US-08-213-151A-2 28 84.6 309 4 US-08-213-150-864A-2 28 84.6 365 2 US-08-920-296-2 28 84.6 365 2 US-08-920-296-2	84.6669 86.6669 86.6669 86.6669 86.6669 86.6669 86.6669 86.6669 86.	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	0
30000000000000000000000000000000000000		22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	44
. 2024年2024年24日202	2 US-08-621-259A-211 Sequence 2 US-08-621-259A-215 Sequence 2 US-08-621-259A-215 Sequence 4 US-09-217-352-219 Sequence 4 US-09-217-352-23 Sequence 6 US-09-079-347-2 Sequence 7 US-08-312-202B-2 Sequence 8 US-09-079-347-2 Sequence 9 US-09-075-725-2 Sequence 9 US-08-809-646-2 Sequence 9 US-08-12433-2 Sequence 9 US-09-177-249-246 Sequence 9 US-09-173-151A-12 Sequence 1 US-08-236-918A-2 Sequence 1 US-08-236-918A-2 Sequence 1 US-08-674-612-2 Sequence 1 US-08-674-612-2 Sequence 2 US-08-746-788-2 Sequence 2 US-08-746-788-2 Sequence	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	
2 US-08-621-259A-211 2 US-08-621-259A-215 4 US-09-217-352-223 4 US-09-217-352-223 2 US-08-312-202B-2 3 US-08-312-202B-2 3 US-08-717-572-2 5 US-08-809-646-2 9 US-09-175-725-2 4 US-09-177-249-246 4 US-09-177-249-246 4 US-09-173-151A-12 4 US-09-173-151A-12 4 US-09-173-151A-2 1 US-08-236-918A-2 1 US-08-150-864A-2 2 US-08-674-612-2 2 US-08-746-788-2	-08 -621 -259A -211 Sequence -08 -621 -259A -215 Sequence -09 -217 -352 -219 Sequence -09 -217 -352 -231 Sequence -09 -217 -352 -231 Sequence -09 -07 -352 -231 Sequence -09 -07 -725 -2 Sequence -09 -07 -725 -2 Sequence -09 -07 -725 -2 Sequence -09 -17 -1243 -2 Sequence -09 -17 -151A -1 Sequence -09 -17 -151A -1 Sequence -09 -17 -151A -2 Sequence -09 -17 -151A -2 Sequence -09 -150 -864A -2 Sequence -09 -150 -864A -2 Sequence -08 -674 -612 Sequence -08 -674 -612 Sequence -08 -674 -616 -2 Sequence -08 -746 -788 -2 Sequence -08 -746 -788 -2 Sequence	365	365	365	309	309	160	120	100	46	46	46	46	46.	9	9	9	9	4
US-08-621-259A-211 US-08-621-259A-215 US-09-621-352-219 US-09-217-352-223 US-09-217-352-223 US-09-079-447-2 US-09-079-447-2 US-09-079-448-2 US-09-173-151A-6 US-09-173-151A-2 US-08-240-246-2 US-08-674-612-2 US-08-674-6788-2	-08 -621 -259A -211 Sequence -08 -621 -259A -215 Sequence -09 -217 -352 -219 Sequence -09 -217 -352 -231 Sequence -09 -217 -352 -231 Sequence -09 -07 -352 -231 Sequence -09 -07 -725 -2 Sequence -09 -07 -725 -2 Sequence -09 -07 -725 -2 Sequence -09 -17 -1243 -2 Sequence -09 -17 -151A -1 Sequence -09 -17 -151A -1 Sequence -09 -17 -151A -2 Sequence -09 -17 -151A -2 Sequence -09 -150 -864A -2 Sequence -09 -150 -864A -2 Sequence -08 -674 -612 Sequence -08 -674 -612 Sequence -08 -674 -616 -2 Sequence -08 -746 -788 -2 Sequence -08 -746 -788 -2 Sequence	Ν	N	1 -4	4	ب	4	4	4	σ	4	ω	ω	N	4	4	N	N	
		US-08-746-788-2	US-08-920-296-2	US-08-674-612-2	US-09-150-864A-2	US-08-236-918A-2	US-09-173-151A-6	US-09-173-151A-12	US-09-177-249-246	PCT-US95-12433-2	US-08-809-646-2	US-09-075-725-2	US-09-079-347-2	US-08-312-202B-2	US-09-217-352-223	US-09-217-352-219	US-08-621-259A-215	US-08-621-259A-211	C27-C00-T70-00-C0

ALIGNMENTS

```
; STRANDEDNESS:
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-881-971-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-881-971-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6013764
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,455
FILING DATE: 17-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: MCN-586
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 908-524-2808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPOSITION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thaier, Adrian
APPLICANT: Villani, Frank J.
TITLE OF INVENTION: LIQUID PHASE PEPTIDE
TITLE OF INVENTION: PULMONARY SURFACTANT
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-524-2641
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: YUB J. TELEPHONE: Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One Johnson CITY: New Brunswick
                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/881,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRY: USA
08933-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Application US/08881971 6013764
                                                                                                                                                                                          amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One Johnson & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maryanoff,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eggmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abdel-Magid, Ahmed F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson & Johnson
                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Urs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cynthia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHESIS OF KL-4
PROTEIN
```

100.0%;

```
DЬ
                                                                                   US-08-881-971-5
                                                                                                       RESULT
                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: US-08-881-971-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-881-971-6; Sequence 6, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                Sequence 5, Application US/08881971 Patent No. 6013764 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/801/...
APPLICATION NUMBER: US/08/801/...
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 60/021/455
APPLICATION NUMBER: US 60/021/455
FILING DATE: 17-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: DOW, KENNETh J.
NAME: DOW, KENNETh J.
NAME: BOW, KENNETh J.
NAME: 32,890
                                                                                                                                                                                                                Query Match 100.0%; Score 26; DB 3; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908-524-2808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abdel-Magid, Anneu r.
APPLICANT: Eggmann, Urs
APPLICANT: Maryanoff, Cynthia A.
APPLICANT: Thaler, Adrian
APPLICANT: Villani, Frank J.
TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-524-2641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 900 --
TELEPHONE: 908-524-2808
TO TO NO:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                         3 KLLLLK 8
                                                                                                                                                                                       1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08933-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08881971 6013764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
Abdel-Magid, Ahmed F. Eggmann, Urs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One Johnson & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.7e+05; Mismatches 0;
                                                                                                                                                                                                                                                DB 3; Length 8
                                                                                                                                                                                                            ; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-881-971-5
                                                                                                                                                                                                                                                                                                                                                                                           US-08-881-971-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATE: 17-JULTICATE ATTORNETY AGENT INFORMATION:
ANTORNETY AGENT INFORMATION:
NAME: DOW, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: MCN-586
TELECOMMUNICATION INFORMATION:
"FTLEPHONE: 908-524-2641
                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 908-524-2808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                    APPLICANT: Abdel-Magid, Ahmed F.
APPLICANT: Eggmann, Urs
APPLICANT: Maryanoff, Cynthia A.
APPLICANT: Maryanoff, Cynthia A.
APPLICANT: Thaler, Adrian
APPLICANT: Tiller, Adrian
TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson STREET: One Johnson & Johnson Plaza CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Maryanoff, Cynthia A.
APPLICANT: Thaler, Adrian
APPLICANT: Villani, Frank J.
TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
                                      COUNTRY: USA
ZIP: 08933-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 908-524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KLLLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Johnson & Johnson Plaza CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:

    Application US/08881971
    6013764

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08933-003
                                                                               New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 26; DB 3; 100.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/881,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ت</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
```

밁

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

SOFTWARE:

PatentIn Release #1.0, Version #1.30

US/08/881,971

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible YSTEM: PC-DOS/MS-DOS

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-07-715-397A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-881-971-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07715397A Patent No. 5260273
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 908-524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,455
FILING DATE: 17-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REGISTRATION NUMBER: 32,890
                                NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163 REFERENCE/DOCKET NUMBER: SCITELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PC-LOASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 908-524-2641
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cochran, Charles G
APPLICANT: Revak, Susan D
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN AND RELATED
TITLE OF INVENTION: POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 19910614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: The Scripps Research Institute, ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KLLLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                     92037
                                                                                                                                                                                                                                                                                                                                                    La Jolla
: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                        3366 No. 5260273th Torrey Pines Ct., Suite 240
                                                                                                                                                                                                                                                                                                                                    USA
                     619-554-6312
                                                                                                                                                                                    US/07/715,397A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCN-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                          SCR0395P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 3; Length 18; Pred. No. 6.4;
                                                                                                                                                                                                                         Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
```

В

1 KLLLLK 6

```
Q
                       Query Match
Best Local Similarity
Tatches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
****hes 6; Conserva
                                                                                                    ; FRAGMENT TYPE: US-08-060-833-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-060-833-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-715-397A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08060833 Patent No. 5407914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN AND RELATED TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cochrane, Charl APPLICANT: Revak, Susan D
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 1066 No. 5407914th Torrey Pines Road, TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                          92037
                                                                                                                                                                                 H: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMINO ACID
Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                    100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                       619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cochrane, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO
                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . peptide
                                                                                                                                                                                                                                                     619-554-2937
                                                                                                                                          : peptide
                                                                                                                                                                                                                                                                                                                                                19930512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                              us/08/060,833
                                                                                                                                                                                                                                                                                         33,950
                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                              SCR1309P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26;
Pred. No.
                                                Score 26;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
. 7.5;
                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                            Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

-08-735-171-1

quence 1, Application US/08735171 tent No. 5741891

```
밁
                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                               US-08-419-824-1
                                                                                                                                                                                                                                           Sequence 1, Application US/08419824 Patent No. 5789381 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 908-524-2808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          APPLICANT: Cochrane, Charles G
APPLICANT: Revak, Susan D
TITLE OF INVENTION: PULMONARY SUI
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Weber, James V.
APPLICANT: Kasulanis, Charles F.
APPLICANT: Sampino, Keith
TITLE OF INVENTION: PULMONARY SURF
TITLE OF INVENTION: SOLUBILIZATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                             STATL.
COUNTRY: U. 92037
                                                                      STREET: LUCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-524-2641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                       ADDRESSEE: Patent Counsel
STREET: 10666 No. 5789381th Torrey Pines Road, TPC 8
                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: OR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/735,171
FILING DATE: 22-OCT-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                              KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08933-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Brunswick
                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One Johnson & Johnson Plaza
                                                                                                                       The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                   PULMONARY SURFACTANT PROTEIN AND RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PULMONARY SURFACTANT PEPTIDE SOLUBILIZATION PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORT-0812
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 21;
7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
```

0,

linear

```
Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
""" 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-826-261-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: US-08-419-824-1
                                                                            APPLICATION NUMBER: US/08/826
FILING DATE: 6-March-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Kenneth J.
REGISTRATION NUMBER: 32,890
REFERENCE/DOCKET NUMBER: ORT-
TELECOMMUNICATION INFORMATION:
TELECHHONE: 732-524-2641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08826261 Patent No. 5952303
                                               TELEFAX: 732-524-2808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, N. Adeyinka
TITLE OF INVENTION: LYOPHILIZED PULMONARY SURFACTANT PEPTIDE COMPOSITIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bornstein, APPLICANT: Williams,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Johnson CITY: New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                        STATE: New
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Logan, April C
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/060,833 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 11-APCLASSIFICATION: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                           08933-003
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   One Johnson & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bornstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                        Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 26; DB 1; 100.0%; Pred. No. 7.5;
                                                                                                                                                                                                                US/08/826,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/419,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.
                                                                                                                  ORT-0822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSRI 147.2CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
```

Score 26; Pred. No. 7

Ψ

Length 21;

```
ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: US-08-826-261-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-848-580-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08848580 Patent No. 6013619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cochrane, Charl
APPLICANT: Revak, Susan D
                                                                          TELEFAX: 619-784-9399
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        APPLICATION NUMBER: US 07 FILING DATE: 04-JAN-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,397
PRIOR DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/488,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-APR-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                     REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                     TELEPHONE:
                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               La Jolla
                            amino acid
 TYPE:
                                                                                                                                                                   Fitting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10550 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                            21 amino acids
                                                                                          619-784-9399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cochrane, Charles G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                 linear
                                                                                                        619-784-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                    11-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
peptide
                                                                                                                                                                                                   06-JAN-1988
                                                                                                                                                                                                                                                                                                                                       12-MAY-1993
                                                                                                                                                                   Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCRIPPS RESEARCH INSTITUTE
NO. 6013619th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THERAPEUTIC USES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL PULMONARY SURFACTANTS AND THERAPEUTIC USES, INCLUDING PULMONARY LAVAGE
                                                                                                                                                                                                                US 07/141,200
                                                                                                                                                                                                                                                                                                                                                                                                US 08/419,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/848,580
                                                                                                                                                                                                                                                           US 07/293,201
                                                                                                                                                                                                                                                                                                                                                  US 08/060,833
                                                                                                                                                   34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                       TSRI 147.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
"~+~hes 6; Conserv:
                                                                                                                        В
                                                                                                                                                                                                                                                           ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-881-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-881-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                          PCT-US92-04537-7
                                                                           RESULT
                          Sequence 7, Application PC/TUS9204537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08881971 Patent No. 6013764
                                                                                                                                                                                    Matches
                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 908-524-2808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Dow, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Villani, Frank J.
TITLE OF INVENTION: LIQUID PHASE PEPTIDE SYNTHESIS OF KL-4
TITLE OF INVENTION: PULMONARY SURFACTANT PROTEIN
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/021,455 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLLK 6
                                                                                                                                                  1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Brunswick
                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08933-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    One Johnson
                                                                                                                                                                                                                                                                                                                                     21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
Cochrane, Charles G
Revak, Susan D
                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                   908-524-2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eggmann, U
Maryanoff,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thaler, Adrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abdel-Magid, Ahmed F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson & Johnson
                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                 908-524-2641
                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                               100.0%; Score 26; DB 3; Length 21; 100.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/881,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cynthia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     & Johnson Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                            32,890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               MCN-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                  0,
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                  0;
```

```
; TOPOLOGY: linear; MOLECULE TYPE: peptide pCT-US92-04537-7
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-920-281C-2
                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07920281C
Patent No. 5739026
Patent No. 5739026
GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
TITLE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PATENTIN REL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,397
FILING DATE: 14-JUN-1991
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 North Torrey Pines Road, Mail Drop TPC8 CITY: La Jolla STREE: California
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: SCI
                                                                                                                                                                                           STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bingham, Douglas A REGISTRATION NUMBER: 32,
APPLICATION NUMBER: US/07/920,281C FILING DATE: 13-AUG-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLLLLK 6
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92037
                                                                                                                                                                  22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMINO ACID
                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19920601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNTHETIC PULMONARY SURFACTANT PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/US92/04537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCR1025P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; I
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
```

뮰 δÃ

```
US-07-920-281C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-466-277-2

Sequence 2, Application US/08466277

Sequence 190666

Patent No. 6190666

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
SEQUENCE DESCRIPTION: SEQ ID NO: US-08-466-277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MULTPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1863 KLLLLK 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: , 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/920,281
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA Expression Systems Based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Garoff, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box 74
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              828-103P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

```
; STRANDEDNESS: single
; TOPQLOGY: linear
; IMMEDÎATE SOURCE:
; LIBRARY: PROSNOT20
; CLONE: 1817518
US-09-088-549-1
                                                                                                                            Query Match
Best Local Similarity
""trhes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
"---hes 6; Conserve
Search completed: June 17, 2002, 12:42:04 Job time: 224 sec
                                                                              망
                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-088-549-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09088549 Patent No. 6231853 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0530 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-855-0572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1863 KLLLLK 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: CORLEY, NEIL C.
APPLICANT: PATTERSON, CHANDRA
TITLE OF INVENTION: HUMAN GLUTATHIONE PEROXIDASE-6
NUMBER OF SEQUENCES: 3
                                                                           1 KLLLLK 6
||:|||
178 KLILLK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/088,549 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Por CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLLK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                          SS: single
linear
                                                                                                                                                             92.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 26; DB 4; I
100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0;
                                                                                                                                          Score 24; DB 4; Length 187; Pred. No. 1.8e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                            0;
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                            0;
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                   3
5
5
7
7
10
11
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
DB
                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                 100.0
           100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1980.DAT: *
2: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1981.DAT: *
3: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1982.DAT: *
3: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1982.DAT: *
4: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1983.DAT: *
4: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1983.DAT: *
5: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1985.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1985.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1985.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1986.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1986.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1989.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1990.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1991.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1991.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1991.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1992.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1993.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1995.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1996.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-emb1\AA1999.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseq\g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       June 17, 2002, 12:41:22; Search time 94.14 Seconds (without alignments) 9.439 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-367-714A-29
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                           Length
              122
122
123
123
123
123
                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapext 0.5
        AAW35155
AAW82853
AAB17419
AAW35149
AAW35152
AAW82847
AAW82850
AAW82850
AAW82850
AAB17416
AAB17416
                                                                                                                                                                                                                                                                                                                                           ID
                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
Leu/Lys diastereom Antipathogenic pep Antipathogenic pep Leu/Lys diastereom Leu/Lys diastereom Antipathogenic pep Antipathogenic pep
                                                                                                                                                                                                                                                                                                                                        Description
```

		33333	3 3 3 3 3 3 3 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2 2 2 2 2 2 2 2 2 2 3 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
85.7 85.7 85.7			85.7 85.7 85.7 85.7	
377 413 489 489	284 295 314 315	125 135 205 216 283 284	359 414 11 15 21 21 21	12 13 13 14 14 37 77 77 77 18
22 22 14 16	16 18 22 18	22 22 22 23	19 19 22 22	21 18 19 19 19 19 19 13
AAU16931 ABG21008 ABG2176 AAR42176 AAR76697	AAR75494 AAW20723 AAB43933 AAE03235 AAW19946 ABC29956	AAU17004 AAY97766 ABG29958 AAB08846 AAB60324 AAR75397	AAW81359 AAE10702 AAB97447 AAW77384 AAW62968 AAW62968 AAW63187 AAB60066 AB629957	748 748 748 748 748 748 748 748 748 748
Human novel secret Human novel secret Novel human diagno Murine MDM2. Mus Mouse MDM2 protein		novel apular human an MDM obacte double	Muman alpha-z-3 si Mouse GM3 synthase Peptide nucleic ac Lytic peptide with Minimalist lytic p Membrane active sy KL3 membrane activ Novel human diagno	athoge ereome athoge athoge pepti athoge athoge once of philic

ALIGNMENTS

RESULT AAW35155

14-APR-1998 (first entry)

Leu/Lys diastereomer peptide [D]-L2,4,6-K3L5

AAW35155

AAW35155 standard; peptide;

œ A

Misc-difference Misc-difference Synthetic (YEDA) YEDA RES & DEV CO LTD 20-FEB-1997; 28-AUG-1997 Misc-difference 22-FEB-1996; ₩09731019-A2 96IL-0117223. 97WO-IL00066 Location/Qualifiers /note= /note= "D-form residue" /note= "D-form residue" "D-form residue"

Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.

continuity of an alpha-helical structure

```
RESULT
AAW82853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
"~+~hes 8; Conserv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc invention. The peptides of the invention have: (a) cytolytic activity on cpathogenic cells (pathogens and malignant cells not naturally present in cc the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse can be used to treat infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) cor cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as capricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides concersed resistance to proteolytic degradation. Non-haemolytic, concertainly, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, we resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts
                                                                                                                                                                                                                                                                      Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                        Oren Z,
                                                                                                                                    20-FEB-1997;
                                                                                                                                                               19-FEB-1998;
                                                                                                                                                                                            27-AUG-1998
                                                                                                                                                                                                                    W09837090-A1
                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                    Antipathogenic
                                                                                                     (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                    19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW82853 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                             1998-594464/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||| 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2,
                                                                          Shai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 40; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                  97WO-IL00066.
                                                                                                                                                             98WO-IL00081.
                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 6.4e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

```
RESULT
AAB17419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                       23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                         cytotoxic T ceil lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17419 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breaker moiety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than I and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                            WPI; 2000-350702/30.
                                                                          Feige U,
                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                    04-MAY-2000
                                                                                                                                                                                                                                                  WO200024782-A2
                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix
                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; anta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present peptide is used to produce the agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 klilklik 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                        inhibitor; erythropoietin; thrombopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                       98US-0105371
99US-0428082
                                                                                                                                                                                     99WO-US25044
                                                                           Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126pp; English.
                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35;
Pred. No.
                                                                          Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO:523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                         IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                        interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                         VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
```

Novel composition of matter comprising an pharmacologically active peptides, useful

Fc domain and for treating

and

cancer and

```
RESULT
AAW35149
ID AAW3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Thes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC fc domain, pharmacologically active peptides, and linkers. Where (1) is:

(C (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(C independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2.

(C (L1)c-P1-(L2)d-P2-(L3)e-P3.) or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

(C where P1, P2, P3, and P4 = are each independently sequences of

(C pharmacologically active peptides; L1, L2, L3, and L4 = are each independently

(C independently linkers; and a, b, c, d, e, and f = are each independently

(C or 1, provided that at least 1 of a and b is 1. The composition can

(C have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

(C activities. DNAs, vectors and host cells from the present invention can

(C be used for producing pharmaceutical compositions. The compositions are

(C activities. DNAs, vectors and host cells from the present invention sare

(C activities of an Fc domain (rather than a Fab domain) can provide a longer

(C The use of an Fc domain (rather than a Fab domain) can provide a longer

(C half-life or incorporate functions such as Fc receptor binding, protein

(C honding, complement fixation, and possibly placental transfer. AAA69443

(C to AAA69526 and AAB16955 to AAB19003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                    Leu/Lys diastereomer peptide; infection; therapy; exci-
Honey bee venom; pardaxin; cytolytic activity; cancer;
non-haemolytic; preservative; agricultural produce; ba
agricultural pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35149 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
(YEDA ) YEDA RES & DEV CO LTD
                             22-FEB-1996;
                                                        20-FEB-1997;
                                                                                                                   W09731019-A2
                                                                                                                                                              Modified-site
                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                 Misc#difference
                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               Leu/Lys diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                             96IL-0117223
                                                        97WO-IL00066
                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                              /note=
12
                                                                                                                                                /note-
                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                  "D-form
                                                                                                                                             "C-terminal amide
                                                                                                                                                                          "D-form
                                                                                                                                                                                                        "D-form
                                                                                                                                                                                                                                     "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                               [D]-L3,4,8,10-K4L8.
                                                                                                                                                                                                                                                                                                                                                                                               infection; therapy; excitatory neurotoxin;
                                                                                                                                                                            residue"
                                                                                                                                                                                                         residue"
                                                                                                                                                                                                                                     residue"
                                                                                                                                                                                                                                                                  residue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matter (I) comprising
and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                    bacterial cell lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an
is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

밁

Š

0

```
infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha helical structures) means that the peptides have few if any toxic effects, and those that include D-aa will have increased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Sinc these random copolymers induce total lysis of bacterial cell walls, resistance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oren
                                                                                                                                                                                                                                                                                              pathogenic cells (pathogens and malignant cells not naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The peptides, their complexes and mixtures are used to treat pathogens.
                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Page 39; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shai Y;
  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                           each has a specific spectrum of or particular applications. Since
                                                                                                                                                                                                                                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                              activity
                                                                                                                                                                                                                                                                                                                                                                        in on
```

```
Query Match
Best Local Similarity
Thes 8; Conserve
                                                                                                                                                                                                                                                                                                                                                      AAW35152
                                                                                                                                                                                                                                                                                                                                                                  RESULT
           Misc-difference
                                 Misc-difference
                                                                              Misc-difference
                                                                                                     Misc-difference
                                                                                                                             Misc-difference
                                                                                                                                                    Misc-difference
                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                             agricultural
                                                                                                                                                                                                                         non-haemolytic;
                                                                                                                                                                                                                                   Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer;
                                                                                                                                                                                                                                                                    Leu/Lys diastereomer peptide [D]-K1,5,9,12L2,6,7,11-K4L8
                                                                                                                                                                                                                                                                                            14-APR-1998
                                                                                                                                                                                                                                                                                                                    AAW35152;
                                                                                                                                                                                                                                                                                                                                          AAW35152 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                  υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                             ic; preservative; agricultural produce;
pesticide; cell wall lysis.
                                                                                                                                        /note=
                                                                                                                                                              Location/Qualifiers
/note=
                    'note=
                                            /note=
                                                                   /note=
                                                                                                                /note=
                                                                                          note=
                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
"D-form residue"
                       "D-form
                                                                                                                  "D-form
                                                                                                                                         "D-form
                                             "D-form
                                                                    "D-form
                                                                                            "D-form
                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                       residue'
                                                                                                                  residue"
                                                                                                                                         residue'
                                                                    residue
                                                                                            residue'
                                             residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                         bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
```

```
В
                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This sequence represents a Leu/Lys diastereomer peptide of the CC invention. The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogens and malignant cells not naturally present in CC concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse concentrations (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as concentratives for food, cosmetics and agricultural produce, or as concentratives for food, cosmetics and agricultural produce, or as concentrative for alpha-helical structures) means that the peptides concentrative for alpha-helical structures) means that the peptides concentrated they few if any toxic effects, and those that include D-aa will have concentrated to the proteolytic degradation. Non-haemolytic, concentrated concentration copolymers of pardaxin, each has a specific spectrum of contivity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, since consistence to them is unlikely to dawning.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                      Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                       Synthetic
                                                                                                                        Antipathogenic peptide.
          WO9837090-A1
                                                                                                                                                         19-MAY-1999
                                                                                                                                                                                        AAW82847;
                                                                                                                                                                                                               AAW82847 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9731019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 8; Conser
                                                                                                                                                                                                                                                                                              G
                                                                                                                                                                                                                                                                                                                       1 KLLLKLLK 8
                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                            1997-435088/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Page 40; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 copolymers induce o them is unlikely
                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96IL-0117223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                               .0%;
                                                                                                                                                                                                                                                                                                                                                                             .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "D-form residue"
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                             Score 35; DB Pred. No. 2.6 0; Mismatches
                                                                                                                                                                                                               ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 to develop.
                                                                                                                                                                                                                                                                                                                                                           DB 2.6;
                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                       Length 12;
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                           0,
```

```
RESULT
AAW82850
                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 8
                                                          27-AUG-1998
                                                                                                                     Synthetic
                                                                                                                                                          Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a corresponding amino acid sequence comprising only 1-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                          19-FEB-1998;
                                                                                      WO9837090-A1
                                                                                                                                                     preservative;
                                                                                                                                                                                                                 Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and alpha-helix (comprises L-amino acid residues and alpha-helix (comprises L-amino acid residues) has a net positive charge greater than 1 and has an amino acid sequence such that positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence such that
                                                                                                                                                                                                                                                  19-MAY-1999
                                                                                                                                                                                                                                                                                 AAW82850
                                                                                                                                                                                                                                                                                                          AAW82850 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-594464/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                        ||||||||
5 klliklik 12
                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 105; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                   pesticide;
                       98WO-IL00081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-IL00066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; S
100.0%; F
tive 0;
                                                                                                                                                  fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;/ Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
the
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
```

20-FEB-1997;

```
RESULT
AAW82856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be
                                                                                                                                                                                                                         Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
               Oren
                                                                                                                                     27-AUG-1998
                                                                                                                                                                 WO9837090-A1
                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                        Antipathogenic
                                                                                                                                                                                                                                                                                                                        19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                 AAW82856 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used as disinfectants for destruction of microorganisms, i.e. solutions for wetting contact lenses, as preservatives, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenic cells. The agent is selected from a cyclic derivative of a pertide which has a net positive charge greater than 1, comprises L-mino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification describes a non-haemolytic, cytolytic agent, which is peptide, a complex of bundled peptides, a mixture of peptides or a peptide copolymer. The agent has a selective cytolytic activity on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                            (YEDA ) YEDA RES & DEV CO LTD
                                                                            20-FEB-1997;
                                                                                                        19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                      AAW82856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLKLLK 8
|||||||
5 klllkllk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               8
               2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEDA RES & DEV
               Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106; 126pp; English.
                                                                            97WO-IL00066.
                                                                                                        98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is used to produce the agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .e. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXCCCCCCCCCCCCCCCCCXXXXFFFFXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
            Feige U,
                                                                                                                                                 04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                               Antipathogenic peptide sequence SEQ ID NO:517.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
              Liu C,
```

Š

8

```
continuity of an alpha-helical structure
                                      New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the
                                                                                                                                                                                    WPI; 1998-594464/50
```

peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a pentide which has a continuous control of a complex control of a control of the used as disinfectants for destruction of microorganisms, i.e. is solutions for wetting contact lenses, as preservatives, e.g., it commetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products. cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infection. They may also they may be used in both human and veterinary medicine. They may also infections. may also be

```
1 KLLLKLLK 8
||||||||
5 klllkllk 12
                       8; Conserv
                        Conservative
                             100.0%;
                        0;
                             Score
Pred.
                        Mismatches
                              No.;
                             DB 2.6;
                                    19;
                        0;
                                    Length
                        Indels
                                    12
                        0;
                        Gaps
```

0;

12

A

```
AAB17413 standard; Peptide; 12
31-OCT-2000
(first entry)
```

Modified peptide; therapeutic agent; fusion; Fc domain, verse autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin thrombopoietin; interleukin 1; MMP; inhibitor; erythropoietin; thrombopoietin; inhibitor; erythropoietin; thrombopoietin; inhibitor; erythropoietin; thrombopoietin; inhibitor; erythropoietin; inhibitor; erythropoietin; inhibitor; erythropoietin; thrombopoietin; inhibitor; erythropoietin; erythropoieti Synthetic asthma; thrombosis; pharmaceutical. antagonist;

```
25-OCT-1999;
 99WO-US25044
```

23-OCT-1998; 22-OCT-1999; 98US-0105371 99US-0428082

```
(AMGE-) AMGEN INC
```

Cheetham

Ç

Boone

Claim

39; Page 378; 608pp; English

diseases

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating of

cancer

and

2000-350702/30.

```
AAB17416
II AAB1
XX
AC ACA
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (I) is: CC independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2, -(L4)f-P4 (CC -(L1)C-P1-(L2)d-P2-(L3)e-P3-(D4)F2-P3-(D4)F2-P1-(L2)d-P2-(L3)e-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F2-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P3-(D4)F3-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
WPI; 2000-350702/30
                                                                       Feige U,
                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                    (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; Cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17416 standard; Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                 98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                 99WO-US25044
                                                            Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                            Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
```

1

```
AAB17483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1. (L1)c-P1-(L2)d-P2. (L4)f-P2 -(L3)e-P3-(L4)f-P4 (CC independently selected from -(L1)c-P1. (L2)d-P2-(L3)e-P3-(L4)f-P4 (CC where P1, P2, P3, and P4 = are each independently sequences of CC independently linkers; and a, b, c, d, e, and f = are each independently sequences of CC independently linkers; and a, b, c, d, e, and f = are each independently CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC be used for producing pharmaceutical compositions. The compositions are CC The use of an Fc domain (rather than a Fc receptor binding, protein CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases. CC half-life or incorporate functions such as Fc receptor binding, protein CC a binding, complement fixation, and possibly placental transfer. AAA69443 CC sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
          WPI; 2000-350702/30
                                             Feige U,
                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                        (AMGE-) AMGEN
                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                  W0200024782-A2
                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                 Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17483 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kliikiik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Page 379; 608pp; English
                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                          INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                      99US-0428082
                                                                                                                       98US-0105371
                                                                                                                                                  99WO-US25044.
                                        Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; S
100.0%; F
tive 0;
                                      J,
                                      Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                     TC;
                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
```

```
AAB17485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino. acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; v immunosuppressive; EPO; TPO; CTLA4; mimetLic; IL-1; TNF; antago MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; autoimmune disease; cytostatic; antiasthmatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L1)d-F2-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating autoimmune diseases
Novel composition of matter comprising an Fc domain and
                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                                    WO200024782-A2
                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                 asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17485 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune
                                WPI; 2000-350702/30
                                                             Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                    Antipathogenic peptide sequence SEQ ID NO:589.
                                                                                           (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ر.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conser
                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 401; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                             INC
                                                                                                                        98US-0105371
99US-0428082
                                                                                                                                                                       99WO-US25044
                                                             Cheetham
                                                                                                                                                                                                                                                                                               pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .08;
                                                             ્પ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                              Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                             TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                       Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (I) comprising ers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer and
                                                                                                                                                                                                                                                                                                                                                       antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                         VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an
is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
cc independently selected from -(L1)c-P1, -(L1)d-P2-(L3)d-P3-(L4)f-P4
cc (L1)c-P1-(L2)d-P2-(L3)e-P^3, or (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
cc where P1, P2, P3, and P4 = are each independently sequences of
cc pharmacologically active peptides; L1, L2, L3, and L4 = are each independently
cc independently linkers; and a, b, c, d, e, and f = are each independently
cc or 1, provided that at least 1 of a and b is 1. The composition can
cc have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
cc activities. DNAs, vectors and host cells from the present invention can
cc be used for producing pharmaceutical compositions. The compositions are
cc useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
cc The use of an Fc domain (rather than a Fab domain) can provide a longer
cc half-life or incorporate functions such as Fc receptor binding, protein
cc A binding, complement fixation, and possibly placental transfer. AAA69443
cc to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
cc sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \ensuremath{\mathsf{pharmacologically}} active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc domain, pharmacologically
(X1)a-F1-(X2)b, where: F1 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention describes composition of matter (I) comprising an obarmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active peptides, and linkers. an Fc domain; X1 and X2 = are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             each
```

```
Query Match
Best Local Similarity
""" 8; Conserv
5 klllkllk 12
             1 KLLLKLLK 8
                           Conservative
                                  100.0%;
                           0;
                                  Score 35;
Pred. No.
                            Mismatches
                                  2.6;
                                         DB
                                          21;
                           0
                                         Length 12
                            Indels
                           0;
                           Gaps
                           0;
```

밁 Q

Sequence

12

```
AAW35231
 Diastereomer
                                                      AAW35231;
                                                                             AAW35231 standard; peptide; 13 AA
                           14-APR-1998
peptide [D]-L3,4,8,10-K4L8C
                         (first entry)
```

agricultural Honey bee venom; non-haemolytic; mer peptide; infection; therapy; excitatory neurotoxin; venom; pardaxin; cytolytic activity; cancer; lytic; preservative; agricultural produce; bacterial ce pesticide; cell wall lysis. bacterial cell lysis;

```
Misc-difference
                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                        Misc-difference
(YEDA ) YEDA
                         22-FEB-1996;
                                               20-FEB-1997;
                                                                       28-AUG-1997
                                                                                               NO9731019-A2
 RES
                         96IL-0117223.
                                               97WO-IL00066
                                                                                                                                  /note=
10
                                                                                                                                                                                                                    Location/Qualifiers
 & DEV CO LTD
                                                                                                                     /note=
                                                                                                                                                                    /note=
                                                                                                                                                                                            /note=
                                                                                                                       "D-form residue"
                                                                                                                                                                     "D-form
                                                                                                                                                                                             "D-form residue
                                                                                                                                             "D-form residue"
                                                                                                                                                                     residue"
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a diastereomer peptide of the invention. This created by binding 5 created by binding 5 copies of this sequence to peptide 23 (see AAW35149). The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogens cand malignant cells not naturally present in the body); but (b) no complex of the invention have: (a) cytolytic activity only at a concentration complex of the complex of complex of the complex of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetLic; IL-1; TWF; antagonist; MMP; inhibitor; erythropojettin; thrombopojettin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothellal growth factor; matrix metalloproteinase;
                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                 WO200024782-A2
                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical
                (AMGE-) AMGEN
                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antipathogenic peptide sequence SEQ ID NO:586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide(s) having selective cytolytic activity - against pathogens and malignant cells, but no haemolytic activity, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 49; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                          98US-0105371.
99US-0428082.
                                                                                                                           99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB Pred. No. 2.8

); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
```

0

```
RESULT
AAW82854
                                                                                                                   밁
                                                                                                                                                                 Ωy
                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (Xl)a-Fl-(X2)b, where: Fl = an Fc domain; Xl and X2 = are each CC independently selected from -(Ll)c-Pl, -(Ll)c-Pl-(L2)d-P2.

CC -(Ll)c-Pl-(L2)d-P2-(L3)e-P-3, or -(Ll)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P-3, or -(Ll)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L2)d-P2-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 39; Page 401; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U,
                              15
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                             ||||||||
5 klllkllk.12
                                                                                                                                                                       1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-350702/30
                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham J,
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                   Score 35; DB : Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boone
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TC;
                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                              Length 13;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                           Gaps
```

```
Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
20-FEB-1997;
                                     19-FEB-1998;
                                                                               27-AUG-1998
                                                                                                                       WO9837090-A1
                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                AAW82854;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW82854 standard; peptide;
                                                                                                                                                                                                                                                                                           Antipathogenic peptide
                                                                                                                                                                                                                                                                                                                                        19-MAY-1999
                                                                                                                                                                                                                                                                                                                                     (first entry)
97WO-IL00066
                                       98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                          14
```

New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts

Oren

Z,

(YEDA)

YEDA Shai

RES

& DEV

CO LTD

WPI; 1998-594464/50

```
DЪ
                                                                                                                                                                                                                                                                                                                                 Search completed: June 17, 2002, 12:41:23 Job time: 298 sec
                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                              CC pathogenic cells. The agent is selected from a cyclic derivative of a corpetide which has a net positive charge greater than 1 comprises L-amino CC acid residues and/or D-amino acid residues and comprises an alpha-helix CC breaker molety, or a peptide (or cyclic derivative of this) which CC (comprises L-amino acid residues and D-amino acid residues, has a net CC (comprises L-amino acid residues and D-amino acid sequence such that CC positive charge greater than 1 and has an amino acid sequence such that CC is not found in nature. The cytolytic agents may be used for treatment of CC cancer or for treatment of several diseases caused by pathogens, CC including bacterial, fungal, viral, mycoplasma and protozoan infections. CC They may be used in both human and veterinary medicine. They may also be CC used as disinfectants for destruction of microorganisms, i.e. in CC cosmetic and food industries, as preservatives, e.g., in the CC cosmetic and food industries, as pesticides (e.g. fungicides or cCC bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 106; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           continuity of an alpha-helical structure
                                                                                                                   |||||||||
6 klllkllk 13
                                                                                                                                                              1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                 Ã,
                                                                                                                                                                                                                                 100.0%; Score 35; D
100.0%; Pred. No. 3;
                                                                                                                                                                                                              0;
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                           0;
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                           0;
```

THIS PAGE BLANK (USPTO)

```
Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                ŏ
 score
                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                       is
                                                                                                                                                                                                                                                                                                                                                                                                      seq
                                                                                                                                                                                                                                                                                  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                      PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                               Query
Match
June 17, 2002, 12:42:59 ; Search time 46.42 Seconds (without alignments) 16.560 Million cell up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-367-714A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                               283138 segs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                              Length
238
302
109
296
387
1211
                                                                                                                                                                                                                                               DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapext 0.5
                                                                     T41809
T00067
G96536
T45215
                                                                                                                                                                                                                      E71375
S27846
                              A88601
T51377
F90441
G81436
                                                                                                      T47638
DJNVCP
                                                                                                                                       F71163
A69735
S15349
                                                                                                                                                                                                                                               IJ
                                                               C69057
                                                                                                                                                                                       S68251
                        T48984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WS
                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5
Compugen Ltd
                                                                                           probable oligopept
phage PBSX termina
mdm2 protein - mou
p53-binding protei
hypothetical prote
hypothetical prote
hypothetical prote
bypothetical prote
DNA-directed DNA p
DNA polymerase orf
            hypothetical prote
ABC transporter, A
probable serine/th
hypothetical prote
hypothetical prote
                                                     conserved bacitrac protein Y49E10.8 [
                                                                      transcription regu
                                                                             hypothetical prote hypothetical prote
                                                                                                                                                             hypothetical prote
hypothetical prote
hypothetical prote
                                                                                                                                                                                      phospholipase C, i
                                                                                                                                                                                                          mypornetical prote RNaseP C5 chain -
                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                     hypothetical prote
                                                                                                                                                                                                                               probable ABC trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell updates/sec
      prote
```

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
28	28	28	28	28	28	29	29	29	29	29	29	29	29	29	29
80.0	80.0	80.0	80.0	80.0	80.0	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9	82.9
164	149	138	138	138	118	1941	1846	1223	884	802	753	684	669	641	632
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
T03915	C84053	AD1469	AC1108	S36115	F90459	T30554	T10670	S62011	E86244	G89893	JC7386	E64496	T44681	G85043	AG1547
hypothetical prote	sodium-qlutamate/a	transcription regu	transcription regu	interferon - Japan	hypothetical prote	ubiquitin-protein	hypothetical prote	PHO85 protein - ye	unknown protein, 4	PriA, primosomal p	retinovin - chicke	ATP-dependent RNA	GTP-binding protei	hypothetical prote	transcription anti

```
probable ABC transporter, ATP-binding protein - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24.Jul-1998 #text_change 17-Mar-2000 C;Accession: E71375
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, F. rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, 7. they, L.; Weidman, J.; Smith, H.O.; Venber, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Accession: E71375
A;Accession: E71375
A;Accession: E71375
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                               A; Reference number: S27846
A; Accession: S27846
A; Molecule +---
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
S27846
                                                                                                                                                                                                                                                         hypothetical protein - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27846
R;Woodward, R.; Carden, M.J.; Gull, K.
submitted to the EMBL Data Library, March 1992
                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-302 <WOO>
A;Cross-references: EMBL:M87318; NID:g162176; PID:g162177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: TP0035
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog C;Keywords: ATP
C;Keywords: ATP
F;27-207/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-238 <COL>
A;Cross-references: GB:AE001188; GB:AE000520; NID:g3322282;
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
E71375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
Query Match 91.4%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLLLKLLK 8
||:||||
55 KLVLKLLK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB Pred. No. 32; 1; Mismatches
Score 32; DB
Pred. No. 40;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                    2; Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 238;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAC65030.1; PID:g332
```

0;

Gaps

0,

7 R **≭** ບ

0,

Gaps

```
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_char.
C;Accession: JE0364
R;Kono, M.; Takashima, S.; Liu, H.; Inoue, M.; Kojima, N.; L
Biochem. Biophys. Res. Commun. 253, 170-175, 1998
A;Title: Molecular cloning and functional expression of a fi
                                                                                                                                         JE0364
                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein RC0799 [imported] - Rickettsia conorii (strain Malish 7) C;Bpecies: R1okettsia conorii C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Accession: 697799
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-296 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE006914; PIDN:AAL03337.1; PID:g15619897; GSPDB:GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.00
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: ribonuclease P, protein component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: preliminary: nucleic acid sequence not shown A:Molecule type: DNA
A:Residues: 1-109 <MIY>
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Miyata, M.; Sano, K.I.; Okada, R.; Fukumura, T. Nucleic Acids Res. 21, 4816-4823, 1993 A; Title: Mapping of replication initiation site in A; Reference number: S42116; MUID:94051609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D14982; NID:g416237; PIDN:BAA03619.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mycoplasma capricolum
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change
C;Accession: S42121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
S42121
RNaseP C5 chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                 287
                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                         1 KLLLKLLK 8
                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 KLLIKLIK 106
                                                                                                                                                                                                                                                                                                                                RC0799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLKLLK 8
                                                                                                                                                                                            KILLKILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 KLLLKVLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLLLKLLK
                                                                                                                                                                                                                                                        Similarity 6; Conser
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                            294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma capricolum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
                                                                                                                                                                                                                                                                88.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%;
                                                                                                                                                                                                                                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                         DB
64;
                                         Kojima, N.; Lee, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВВ
                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                   #text_change 11-May-2000
                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                    Length 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
                                                                                                                                                                                                                                        Indels
    fifth-type alpha2,3-sialyltrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capricolum genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g416239
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-Jun-2000
                                      Hamamoto,
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                    Tsuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           two
                                                                                           RESULT
H82873
                                                                                                                                                        밁
                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΩV
```

```
hypothetical protein UU580 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change C;Accession: H82873 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Cher
                  submitted to GenBank,
A:Description: The cor
                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: phosphoric diester hydrolase
F;314-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain
F;543-663/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
A; Residues: 284-292, 'X', 294-296, 'R'; 568-577; 751-753, 'L', 755-759; 765-776, 'T', 778-780; 8
A; Experimental source: erythrocyte
A; Note: 885-His was also found
C; Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phospha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Experimental source: erythrocyte
R:Waldo, G.L.; Morris, A.J.; Klapper, D.G.; Harden, T.K.
Mol. Pharmacol. 40, 480-489, 1991
A:Title: Receptor- and G-protein regulated 150-kDa avian phospholipase ished by immunoreactivity and peptide sequence.
A:Reference number: A61270; MUID:92017673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 210-216,'M',218-231;244-248;284-291;345-353,'S',355-360;453-461;661-679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A61270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Molecular cloning,
A;Reference number: S68251;
A;Accession: S68251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phospholipase C, inositol-lipid specific (EC 3.1.4.-) isoform beta C;Species: Meleagris gallopavo (common turkey) C;Date: 05-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 22-C;Accession: S6625j, S72374; A6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U49431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1211 <WALL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Waldo, G.L.; Pa
Biochem. J. 316,
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:Y15003
C;Superfamily: alpha-2,3-sialyltransferase
C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: JE0364
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-387 <KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                           902
                                                                                                                                                                                                                                                                      1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 KFLLKLLK 375
                                                                                                                                                                                                                                  KLFLKLLK 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, enBank, February 2000
The complete sequence of Ureaplasma urealyticum: Alternate views
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S72374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paterson, A.; Bo
6, 559-568, 1996
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                            88.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression and MUID:96257751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boyer, J.L.; Nicholas, R.A.; Harden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID: g1223919; PIDN: AAC60011.1;
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                        Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                        DB 2;
2.5e+02;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STZ
                                                                      #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                    Length 1211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity of G-alpha(11)- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g1223920
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                        Gaps

    turkey

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                      ××
```

Alternate views of a

Mon

Jun

17 15:43:16

Ŋ

```
A;Reference number: A8287
A;Accession: H82873
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: F90392
R; She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Reddarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                          hypothetical protein jhp0431 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: "strain J99
G;Date: 12:Feb-1999 #sequence_revision 12-Feb-1999 #text_change 11-Jan-2000
C;Date: 12:Feb-1999 #sequence_revision 12-Feb-1999 #text_change 11-Jan-2000
C;Accession: G71932
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V
                                         A;Cross-references: GB:AE001477; GB:AE001439; A;Experimental source: strain J99 C;Genetics:
                                                                                                 A;Title: Genomic sequence comparison of two A;Reference number: A71800; MUID:99120557 A;Accession: G71932 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-282 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SSO2227 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: F90392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genetic code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: UU580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE002156; GB:AF222894; NID:g6899580; PIDN:AAF30994.1; GSPDB:GN00:
A;Experimental source: serovar 3; biovar 1
  A; Gene: jhp043:
C; Superfamily:
                                                                                                                                                                                                                           ; Ives, C.; Gibson, R.; M
Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-191 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A99139
A; Accession: F90392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:AE006641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLILRLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALLKLLK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity 75.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
    Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.7%;
75.0%;
hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID: g13815527; PIDN: AAK42397.1; GSPDB: GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
No.
                                                                                                                                                                                                         unrelated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
58;
                                                                                NID:g4154961; PIDN:AAD06012.1; PID:g41549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 191
                                                                                                                                                                                                       isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                D.E.; Vovis, G.
                                                                                                                                                                                                     gastric
                                                                                                                                                                                                                                                                    Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                      U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chan
                                                                                                                                                                                                                                                D.R.
                                                                                                                                                                                                       pat
                                       A; Molecule type: DNA
A; Residues: 1-433 <KUN>
                                                                                A;Status: preliminary; nucleic acid sequence
                   Cross-references:
```

```
A; Gene: PH0507
C; Superfamily: un
C; Keywords: ATP
F; 27-230/Domain:
                                                                                                                                                                                                                                                                                               M.; Ohfuku, Y.; Funahasnı, T.; Iuuman, T., DNA Res. 5, 55-76, 1998

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A:Reference number: A71000; MUID:98344137
                                                                                                                                                                                               A;Cross-references: GB:AP000002; NID:g3236129; A;Experimental source: strain OT3 A;Note: this accession replaces an interim acce C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
밁
                           Ş
                                                                                                                                                                                                                                                                                                                                                                      R;Kawarabayasi, Y.; Sawada, M.; M.; Ohfuku, Y.; Funahashi, T.;
                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 17-Mar-2000
C;Accession: F71163
                                                                                                                                                                                                                                                                                                                                                                                                                                 probable oligopeptide transport ATP-binding protein AppF - Pyrococcus horikoshii
C; Species: Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                             A; Residues: 1-321 <KAW>
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 KIVLKLLK 178
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLLLKLLK 8
                              1 KLLLKLLK 8
KLILRLLK 62
                                                        6; Conserv
                                                                                                                                                                  unassigned ATP-binding cassette proteins;
                                                                                                                                   ATP-binding cassette
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
75.0%;
                                                                         85.
75.
                                                                           .7%;
                                                                                                                                                                                                                                                                                                                                                                      Horikawa, H.; Haikawa,
Tanaka, T.; Kudoh, Y.;
                                                         Score 30; DB
Pred. No. 1.1e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                               interim accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                     homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                                     DB 2,
1.1e+02;
0;
                                                                                                                                                                                                                                             PIDN:BAA29595.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                        Length 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 282
                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                      Y.; Hino,
Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                Ø
                                                                                                                                                                   ATP-binding
                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                               PID:d1030538; PID:g32
                                                                                                                                                                                                                                                                                                                                                                      Y.; Yamamoto J.; Kushida,
                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                               replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                             Gaps
                                                                                                                                                                   cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto,
                                                              0
                                                                                                                                                                                                                by GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                       s
;
                                                                                                                                                                                                                                                                                                                                                                      ) Se
```

```
Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A; A; A; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phage PBSX terminase large CHALL ACC.

C;Species: Bacillus subtilis

C;Species: Bacillus subtilis
```

GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13115.1; PID:e11832 ce: strain 168

not shown; translation

not

Devine,

K.M.; McConnell, D.J

of the induction of PBSX in

Ве

```
A;Cross-references: EMBL:Z12020; NID:g35211; PIDN:CAA78055.1; R;Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M. Nucleic Acids Res. 23, 2584-2592, 1995
A;Title: A functional p53-responsive intronic promoter is cont A;Reference number: S57338; MUID:95380270
A;Accession: S57338
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 176, 5820-5830, 1994
A;Title: Genetic control of bacterial suicide: regu.
A;Reference number: I40408; MUID:94364963
A;Accession: I40415
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-76 <RES>
A;Cross-references: EMBL:Z34287; NID:9498810; PIDN:
                                                                                                                                                                                                                                                        N;Contains: p53-binding protein mdm2, s
C;Species: Homo sapiens (man)
C;Date: 17-Mar 2000 #sequence_revision
C;Accession: S24354; S57338; G02026
A; Molecule
                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-491 <OLI>
                                                                                                                                                                                        A; Title: Amplification of a A; Reference number: S24354;
                                                                                                                                                                                                                          R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, Nature 358, 80-83, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-489 <FAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mdm2 protein - C; Species: Mus
                                                                                                                                                                         A; Accession: S24354
                                                                                                                                                                                                                                                                                                                           p53-binding protein mdm2 - human
N;Alternate names: mdm-2 oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: human p53-binding protein mdm2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X58876; NID:g53038; PIDN:CAA41684.1; PID:g53039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S15349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Tumorigenic potential associated A;Reference number: S15349; MUID:91224107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Fakharzadeh, S.S.; Trusko, EMBO J. 10, 1565-1569, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S15349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 13-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: xtmB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    \mathfrak{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIVLKLLK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 13-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: Z34287; NID: g498810; PIDN: CAA84048.1; PID: g498818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Jr
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%;
75.0%;
                                                                                                                                                                                        gene encoding a MUID:92310576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial suicide: regulation MUID:94364963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.P.; George,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB
Pred. No. 1.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB; Pred. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                         mouse double minute 2 homolog; p53-associated m2, splice form A \,
                                                                                                                                                                                                                                                                         17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2,
1.5e+02;
0;
                                                                                                                                                                                                      p53-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; L
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change
                                                                                                                                                                                                                                                                       #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 433
                                                                                                                                                                                                                                     D.L.; Vogelstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
                                                                contained within
                                                                                                                                                                                                      protein
                                                                                                               PID:g35212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                      in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a gene that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        ₩.
                                                                the
                                                                                                                                                                                                      sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                human
                                                                                                                                                                                                                                                                                                                         phospho
                                                                mdr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            am
```

```
C; Accession: T47638
R; Obermaier, B.; Ottenwae
submitted to the Protein
                                                                                                                                                                                              RESULT
T47638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Map position: 12q14.3-12q15
C;Superfamily: human p53-binding protein mdm2
C;Superfamily: human p53-binding protein mdm-2
C;Keywords: alternative splicing; oncogene; phosphoprotein
F;1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #s
A; Molecule type: DNA
A; Residues: 1-727 <0
                                                   A; Reference number: A; Accession: T47638
                                                                                                                      hypothetical protein T5N23.150 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #tc:Accession: T47638
                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SPAC6C3.07 - fissi
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision
C;Accession: T39031
                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SPDB:SPAC6C3.07
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z69731; PIDN:CAA93619.1; GSPDB:GN00066; A;Experimental source: strain 972h-; cosmid c6C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Devlin, K.; Churcher, C.M.; submitted to the EMBL Data Lil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-515 <DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z21750
A; Accession: T39031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-16,'P',18-24 <ZAU>
A;Cross-references: EMBL:U28935; NID:g904033; PIDN:AAA82237.1; PID:g904034
R;Lunec, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:250456;
A; Map position: 12q14.3-12q15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB:MDM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-27,223-491 <LUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library A; Description: Multiple alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: G02026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LLLKLLK 8
||||||
33 LLLKLLK 39
                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                    1 KLLLKLLK
                                                                                                                                                                                                                                                                     KLLLKLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source: splice
                                                                                                       Ottenwaelder, B.;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U33199; NID: g992676; PIDN: AAA75514.1; PID: g992677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G09070
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                        85.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library, August 1995
ternate spliced mdm2
                                                                                                                                                                                                                                                                                                                                                      . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMIM: 164785
                                                                                                                                                                                                                                                                                                                                    Score 30; DB
Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                       Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30;
Pred. No.
                                                                                                    Duchemin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                         20-Apr-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-Dec-1999 #text_change 03-Dec-1999
                                                                                       March
                                                                                                                                                                                                                                                                                                                                                    DB 2;
1.8e+02;
                                                                                                         .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rajandream,
1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcripts
                                                                                                       Zeitler,
                                                                                       2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                     Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with
                                                                                                     Mewes, H.W.; Lemcke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walsh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loss
                                                                                                                                         20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPDB:SPAC6C3.07
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of p53 binding
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
```

THIS PAGE BLANK (USPTO)

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq
   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                             Query
Match
  BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-367-714A-29
35
1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 17, 2002, 12:44:46 ; Search time 21.35 Seconds (without alignments)
14.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                             SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                              Length
  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapext 0.5
Y035_TREPA
RNPA_MYCCA
XTMB_BACSU
MDM2_CANFA
MDM2_CANFA
MDM2_HUMAN
VD56_SCHPO
GGA3_HUMAN
VD56_STAAU
DPOL_NPVBM
CAPG_STAAU
SOML_STAMU
SOML_SPAAU
SOML_SIGGU
UBRL_KLULA
RL18_TRYBB
IPLL_YEAST
ASG2_BACSU
HE47_DROME
YPNP_BACSU
HE47_DROME
YPNP_BACSU
HE47_DROME
YFAS_STAAU
ASPA_BACSU
HE47_DROME
YPNP_BACSU
HE47_DROME
YFAS_STAAU
ASGACSU
YC42_SYNY3
AAAT_RABIT
AAAX_BACSU
YC530_HELPY
YC30_HELPY
YC30_HELPY
YC30_HELPY
YC30_HELPY
YC31_SYNY3
DPO3_BACSU
YC31_SYNY3
                                                                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105224
083078 treponema p
p43039 mycoplasma
p39786 bacillus su
p56950 canis famil
p23804 mus musculu
p56951 equus cabal
000987 homo sapien
010310 schizosacch
091052 homo sapien
p18131 autographa
p41712 bombyx mori
p39856 staphylococ
091944 tetraodon m
p54863 sparus aura
p79894 sparus aura
09ygk7 sciaenops o
09pwg4 siganus gut
060014 kluyveromyc
p50885 trypanosoma
p38991 saccharomyc
034482 bacillus su
027268 drosophila
p54181 bacillus su
027268 pynechocyst
019105 mus musculu
0472349 spacillus su
p42349 spacillus su
p4349 spacillus su
p51912 mus musculu
045493 bacillus su
p51915 mus musculu
045493 bacillus su
p51916 helicobacte
p92116 helicobacte
p92116 bacillus su
p55785 synechocyst
                                                                                                                                                                                                                                                                                                            Description
```

DR DR DR DR SQ SQ	4888888888888888888888888888888888888	RA R	OCC OCC DIT	1 !
EMBL; AEC TIGR; TPG InterPro; InterPro; InterPro; Pfam; p; PROSITE; Hypotheti Complete NP_BIND SEQUENCE	Science -!- FUNC TPUNC TPUNC TOUP -!- SUBC -!- SIMI This SWI between the Euro use by modified entities or send	SEQUENCE J SEQUENCE J STRAIN-NI MEDLINE-99 Fraser C.1 Dodson R. Dodson R. Sodergren Khalak H. McDonald J Hatch B., Venter J.("Complete "Complete"	RESULT 1 Y035_TREP; ID Y035_TREP; AC 083078; DT 16-0CT-200 DT 16-0CT-200 DT 16-0CT-200 DE Probable r Probable r TP0035. GN TP0035. GN TREPONEMA OC BACTETIA; OX NCBL_TAXII	365 444 440 443 443 443
AEO TPO Pro; Pro; PFO TE; heti heti ete ND ND	Science 28:375-388(1998 1- FUNCTION: PART OF AM	SEQUENCE FROM N.A STRAIN-NICHOLS; MEDLINE-98332770; Fraser C.M., Norr Dodson R., Gwinn Sodergren E., Har Knalak H., Richar McDonald L., Arti Hatch B., Horst K Hatch B., Horst K Venter J.C.; "Complete genome	UT 1 705_TREPA STANDARD; 983078; 16-0CT-2001 (Rel. 40, Cr. 16-0CT-2001 (Rel. 40, La. 16-0CT-2001 (Rel. 40, La. 16-0CT-3001 (Rel. 40, Cr. 16-0CT-3001	27 27 27 27 27 27 27 27
001188; AAC6; 001188; AAC6; 01503439; 015000687; 010005; AB_ELT PS00211; AB_ELT PS00211; AB_CCal proteome. 44 4 238 AA; 238 AA;	281:375-388 TITION: DAYT 34/TP0035/T 34/TP0035/T ELLUG TO THE ELLUGR TO	ROM N.A. HOLS; [332770; pubMe] [, Norris S.J. Gwinn M., Hi E., Hardham J Richardson D Richardson P L., Artiach P Horst K., Rob L; genome sequen	A STAND Ol (Rel. 40 Ol (Rel. 40 Ol (Rel. trans metal trans pallidum. Spirochaet	777.1
ABC_ ATP_ Can; Can; CTRA CTRA Tra 26460	FUNCTION: PART OF AN ATP-DRIV FUNCTION: PART OF AN ATP-DRIV TP0034/TP0035/TP0036 FOR A ME COUPLING TO THE TRANSPORT SYS SUBCELLULAR LOCATION: Inner m SIMILARITY: BELONGS TO THE AB SIMISS-PROT entry is copyrigh ween the Swiss Institute of E European Bioinformatics Insti by non-profit institutions fied and this statement is no ties requires a license agree end an email to license@isb.s-	PubMed=966587 Pis S.J., Weins M., Hickey E.K dham J.M., McL ddson D., Howel ach P., Bowman C., Roberts K., sequence of Tr	, ste	1180 1 1285 1 342 1 346 1 366 1 431 1 431 1 470 1
30.1; BC_transportx TP_GTP_A. ; 1. TRANSPORTER; Transport; In Transport; ATP (P	p-DR: R A N RRT SI nner THE N THE N Institution	SEQUENCE FROM N.A. STRAIN=NICHOLS; MEDLINE=9832770; PubMed=9665876; MEDLINE=9832770; PubMed=9665876; Fraser C.M., Norris S.J., Weinstock G.M., Dodson R., Gwinn M., Hickey E.K., Clayton Sodergren E., Hardham J.M., McLeod M.P., Khalak H., Richardson D., Howell J.K., Ch McDonald L., Artiach P., Bowman C., Cotto McConald L., Artiach P., Bowman C., Cotto Hatch B., Horst K., Koberts K., Sandusky Venter J.C.; "Complete genome sequence of Treponema pa spirochete.";	PRT; 238 A ted) sequence update annotation upda ystem ATP-bindin Spirochaetaceae;	RNPA_MYCGE YD65_SCHPO LP61_EINTE Y755_METJA ETFA_YEAT YC89_ARCFU YAHA_ECOLI RMAR_HANNI YQAT_BACSU Y610_METJA YCHB_BACSU GLG1_SOLTU GLG1_SOLTU
sportr. A. RTER; FALSE_NEG. rt; Inner membrane; ATP- rt; (POTENTIAL). 673E7B4882BE4D29 CRC64	PROBABLY R ane-associa ane-associa ANSPORTER F tisproduc formatics formatics There ar long as it mmoved. Use Mose http:	White O., R., Ketchu R., Ketchu Salzberg S. idambaram M n M.D., Ful M., Weidman	A.) te) g protein	A_MYCGE 5_SCHPO 1_EIMTE 6_NETJA A_RCFU 9_ARCFU A_ECOLI T_BACSU 0_METJA B_BACSU 1_SOLTU 1_SOLTU
binding;	EM PONSIBLE FOR ENE d (Potential). IILY. through a colla d the EMBL outs no restrictions content is in by and for col www.isb-sib.ch/a	Sutton G.G m K.A., , Peterson ., Utterba ii C., Gar J., Smith	TP0035.	P47703 Q10317 P15714 Q58165 Q124165 Q128980 028980 P21514 P41814 P48849 P45916 Q58027 Q58027 Q00081
·	STEM ESPONSIBLE FOR ENERGY ted (Potential). AMILY. AMILY. ed through a collaboration and the EMBL outstation e no restrictions on its content is in no way ge by and for commercial //www.isb-sib.ch/announce/	G.G., son J., rback T., Garland S., ith H.O.,		mycoplasma schizosacch eimeria ten methanococc saccharomyc archaeoglob escherichia hansennla w bacillus su methanococc bacillus su solanum tub

Query Match 91.
Best Local Similarity 87.
Matches 7; Conservative

91.4%;

Score 32; DB Pred. No. 11; 1; Mismatches

1; 0;

Length 238; Indels

0;

밁 Š

KLVLKLLK KLLLKLLK 8

62

```
RESULT 2
RNPA_MYCCA
ID RNPA_M
AC P43039
DT 01-NOV
DT 01-NOV
DT 16-OCT
DE RIDDNI
DE RIDDNI
DE RIDDNI
CRASC
GN MYCOPI
OC BACCEC
OX MYCOPI
OC COC NOBLI
RN [1]
RN [1]
RN HEDLIN
RN MEDLIN
RN MYADLI
RN MYADLI
RN MYADLI
RN MYADLI
CC -!- FT
CC C C C
CC C
CC C C
CC C
C
C
C
C
C
C

                                    ID AC DT DT DT DT DT
                                                                                                                                                                                                          RESULT 3
XTMB_BACSU
                                                                                                                                                                                                                                                                                                                               뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RX MEDLINE=94051609; PubMed=8233831;
RA Miyata M., Sano K.-I., Okada R., Fukumura T.;
RT "Mapping of replication initiation site in Mycoplasma capricolum genome by two-dimensional geli-electrophoretic analysis.";
RT genome by two-dimensional geli-electrophoretic analysis.";
RT Nucleic Acids Res. 21:4816-4833(1993).
CC From pre-tina to produce the mature 5'termins. It can also component plays an auxiliary but essential role in vivo by binding component plays an auxiliary but essential role in vivo by binding to the 5'-leader sequence and broadening the substrate specificity of the 5'-leader sequence and broadening the substrate specificity cof the ribozyme (By similarity).
CC Of the ribozyme (By similarity) cleavage of RNA, removing 5'-cafalyTTC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-correction consists of a catalytic RNA component (M1 or rnpB) and a rectain enhant (RN esimilarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                       01-FEB-1995
01-OCT-1996
16-OCT-2001
                           PBSX phage
                                                                                                                                                XTMB_BACSU
P39786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00825; Ribonuclease_P; 1.
PROSTTE; PS00648; RIBONUCLEASE_P; 1.
Hydrolase; Nuclease; Endonuclease; tRNA processing; RN
SEQUENCE 109 AA; 12900 MW; ACF520A0982C0D12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D14982;
HSSP; P25814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P43039;
01-NOV-1995 (
01-NOV-1995 (
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease P protein component (EC 3.1.26.5)
(RNase P protein) (Protein C5).
                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entomoplasmataceae.
NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma capricolum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNPA_MYCCA
                                                                                                                                                                                                                                                                                                                                                                          1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                |||:||:|
|||:||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein subunit (By similarity).
SIMILARITY: BELONGS TO THE RNPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000100; Ribonuclease_P.
(Rel. 31, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
terminase large subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1A6F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAA03619.1; -.
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 1;
Pred. No. 8.2;
Pred. No. 8.2;
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                            433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RNaseP protein)
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

. 1

```
RESULT 4
MDM2_CANFA
                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                             Ъ
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 6
            canine and equine homologues of proto-oncogene.";
                                                         SEQUENCE OF 1-484 FROM N.A.
MEDLINE=20218866; PubMed=10754200;
Nasir L., Burr P.D., McFarlane S.T.,
Cancer
[2]
                                                                                                         Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAR-2002 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).
                                                                                                                                                                                                                          MDM2_CANFA
P56950;
                                                    Nasir L., Burr P.D.,
Argyle D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            DNA packaging;
SEQUENCE 433
                                                                                                                                                                                                                                                                                                                                                                                                              SubtiList; BG11000; xtmB.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z70177; CAA94059.1;
EMBL; Z34287; CAA84048.1;
EMBL; Z99110; CAB13115.1;
EMBL; Z99110; CAB13115.1;
EMBL; S47115; S47115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XTMB.

Bacillus subtilis.

Bacteria, Firmicutes; Ba
Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94364963; PubMed=8083174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-76 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krogh S., O'Reilly M., Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                           39 KIVLKLLK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                              1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. AA; 51150 MW; 47
                                                                                                                                                                                                                                                                                                                                             85.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nolan N., Devine K.M.;
o the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                    ?
                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                        expression of the cDNAs encoding the mouse double minute 2 (mdm2)
                                                                                                                                                                                                                                                                                                                                                                                  471FC77DFEA2CA10 CRC64;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                          Gault E.,
                                                                                                                                                                                                                                 487
                                                                                                                                                                                                                                                                                                                                            DB 1;
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group;
                                                       Thompson
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                    Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
                                                         н.,
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                            0;
```

SEQUENCE FROM N.A. (ISOFORMS MDM2 MEDLINE=20065171; PubMed=10597303

(ISOFORMS MDM2 AND MDM2-ALPHA).

Matches

Conservative

0;

Mismatches

0,

Indels

0,:

Gaps

0;

100.0%; 85.7%;

Score 30; Pred. No.

DB 57;

۲.

Length 487

Query Match Best Local Similarity

```
VARSPLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; pF02279; MDM2; 1.
pfam; pF00641; zf-RanBP; 1.
sMART; SM00184; RING; 1.
sMOSITE; pS01358; zF-RANBP2_1; 1.
pROSITE; pS50199; zF-RANBP2_2; 1.
pROSITE; pS50199; zF-RANBP2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vitro and disrupts the p53-binding domain of mdm2 protein.";
Oncogene 18:7026-7033(1999).
-i- FUNCTION: INHBUTS D53- AND P73-MEDIATED CELL CYCLE ARREST AND APOPTOSIS BY BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN.
FUNCTIONS AS AN UBIQUITH LIGASE E3, IN THE PRESENCE OF E1 AND TOMARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND TARGETS IT FOR PROTEASOME-MEDIATED PROTEDLYSIS (BY SIMILARITY).
-i- COPACTOR: ZINC IS REQUIRED FOR UBIQUITIN LIGASE E3 ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :-
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF100705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                       Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel exon within the mdm2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Veldhoen N., Metcalfe S., Milner J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN (RB), EIA-ASSOCIATED PROTEIN P300 AND THE E2F1
TRANSCRIPTION FACTOR (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. EXPRESSED
PREDOMINANTLY IN THE NUCLEOPLASM (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; MDM2 (SHOWN HERE) AND MDM2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITSELF (BY SIMILARITY).

SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 RANBP2-TYPE ZINC FINGER.
SIMILARITY: BELONGS TO THE MDM2 / MDM4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1. REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A PUTATIVE C4-TYPE ZINC FINGER, THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH RNA WHETHER OR NOT ZINC IS RESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MDM4. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: MDM2-ALPHA IS PRESENT IN TESTICULAR TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).

SUBUNIT: BINDS P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN FOR POPULATION AND AND PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSO ESSENTIAL FOR ITS UBIQUITIN LIGASE E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UMT8; 1YCR
                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IPR003160; MDM2.
; IPR001876; Znf-Ra
; IPR001841; Znf_r;
                                                                                                                                                                                                                                                                                                              ; Metal-binding; ; 19 108 179 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF67833.1;
                                                                                                                                                                                                                                                                                                                                                                                  ; ZF_RING_2; 1.
Ligase; Ubiquitin conjugation; Oncogene;
                                                                                                                     108
185
202
304
215
215
331
301
328
475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Znf-RanBP
     WW;
                                                                                                                                                                                                                                                                                                                                                           Alternative splicing.
                                                                                                                                            ASP/GLU-RICH RANBP2-TYPE. RING-TYPE.
                         MISSING
G -> D (
                                                                                               NUCLEOLAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                       REGION II.
                                                                                                                                                                                                                                                POLY-SER
                                                                                                                                                                                                                                                                    ARF BINDING.
                                                                                                                                                                                                                                                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL) NUCLEAR EXPORT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                          REGION I
     60CDB470A32A8E69 CRC64;
                                               D (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulates
domain of
                           HH
                                                                      (IN ISOFORM MDM2-ALPHA)
                                                                                                                                                                                           (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation initiation
mdm2 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H MDM4. IT IS
TOWARD P53 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              its
```

```
RESULT
MDM2_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
   В
                                                                                                                                                                                                                 J. Biol.
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDM2_MOUSE STANDARD; PRT; 489 AA.
P23804: Q64330; Q61040;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-)
Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
MEDLINB-91224107; PubMed-2026149;
Fakharzadeh S.S., Trusko S.P., George D.L.;
Pamorigenic potential associated with enhanced that is amplified in a mouse tumor cell line.";
EMBO J. 10:1565-1569(1991).
                                                                                                                                                            MEDLINE=20180080; PubMed=10713: Weber J.D., Kuo M.-L., Bothner Roussel M.F., Sherr C.J.;
                                                                                                                                                                                                                                                                                                               de Oca Luna R.M., Tabor A.D., Eberspac
Worth L.L., Colman M.S., Finlay C.A.,
"The organization and expression of the
Genomics 33:352-357(1996).
                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic organization of Gene 175:209-213(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97074674; PubMed=8917101;
Jones S.N., Ansari-Lari M.A., Han
Donehower L.A., Bradley A.;
                                                            Khosravi R., Maya R., Gottlieb T., O
                                                                                                                         "Cooperative signals governing ARF-mdm2 localization of the complex."; mol. Cell. Biol. 20:2517-2528(2000).
                                                                                                                                                                                                                                        ultraviolet light.
                                                                                                                                                                                                                                                               Saucedo L.J., Myers C
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 MEDLINE=99175199; PubMed=10075719;
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96299630;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-129/SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                         in response to DNA damage.";
Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
                                                                                       MEDLINE=20079591;
                                                                                                                                                                                      NUCLEOLAR LOCALIZATION SIGNAL. MEDLINE=20180080; PubMed=10713175;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                   PHOSPHORYLATION BY ATM.
                                                                                                                                                                                                                                                   "Multiple murine double minute gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLKLLK
                                                                                                                                                                                                                              Chem.
  AS
                                                                                                                                                                                                                              274:8161-8168(1999).
HIBITS P53-AND P73-MEDIATED CELL CYCLE ARREST BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN AN UBIQUITIN LIGASE E3, IN THE PRESENCE OF E1
                                                                                      PubMed=10611322;
                                                                                                                                                                                                                                                                                                                                                                 PubMed=8660994;
                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORM MDM2-P90)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM MDM2-P90).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                              of the
                                                                                                                                                                                                                                                                .D., Perry M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                              mouse double minute
                                                                                                                                                                                                                                                                                                                                                   Eberspaecher H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hancock A.R., Jones W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae.
                                                                                                                                                                          В.,
                                                               Oren
on of
                                                                                                                                                                          DiGiammarino E.L.,
                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                             the mdm2
                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                                                         Lozano
                                                                                                                                                                                                                                                     (MDM2)
                                                               MDM2
                                                                                                                                                   interaction
                                                                                                                                                                                                                                                                                         MDM2-P76)
                                                             Shiloh Y.,
2 precedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae;
                                                                                                                                                                                                                                                     proteins
                                                                                                                                                                                                                                                                                                                            gene.
                                                                                                                                                                                                                                                                                                                                         G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (P53-binding
                                                                                                                                                                                                                                                                                                                                                    Hulboy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                            ٧.,
                                                                                                                                                   and nucleolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae;
                                                               , Shkedy
p53 accu
                                                                                                                                                                                                                                                                                                                                                       Ū
                                                                                                                                                                           Kriwacki R.W.,
                                                                                                                                                                                                                                                      are induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbs
                                                             kedy D.;
accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.A.,
     AND
                                                                                                                                                                                                                                                     Ьy
     E2
```

```
Pfam; PF02279; MDM2; 1.

Pfam; PF02279; MDM2; 1.

Pfam; PF00641; zf-RanBP; 1.

SMART; SM00184; RING; 1.

PROSITE; PS01358; ZF_RANBP2_1; 1

PROSITE; PS50199; ZF_RANBP2_2; 1

PROSITE; PS50518; ZF_RING_1; FALL
                                                                                                                                                                                                                                                                                                   EMBL; V58876;
EMBL; U47944;
EMBL; U47935;
EMBL; U47935;
EMBL; U47937;
EMBL; U47938;
EMBL; U47938;
EMBL; U47939;
EMBL; U47940;
EMBL; U47940;
EMBL; U47941;
EMBL; U47941;
EMBL; U47943;
EMBL; U47943;
EMBL; U47943;
                                                                                                                                                        InterPro; IPR001841;
                                                                                                                                                                              InterPro; IPR003160; MDM2.
InterPro; IPR001876; Znf-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOWARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND TARGETS IT FOR PROTEASOME-MEDIATED PROTEOLYSIS.

-!- COFACTOR: ZINC IS REQUIRED FOR UBIQUITIN LIGASE E3 ACTIVITY. SUBUNIT: BINDS P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN (RB), E1A-ASSOCIATED PROTEIN P300 AND THE E2F1

TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. EXPRESSED PREDOMINANTLY IN THE NUCLEOPLASM. INTERACTION WITH ARF(P14) RESULTS IN THE LOCALIZATION OF BOTH PROTEINS TO THE NUCLEOLUS. THI NUCLEOLAR LOCALIZATION SIGNALS IN BOTH ARF(P14) AND MDM2 MAY BE DEFORMED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE THYMUS, SPLEEN, AND INTESTINE, THE LEVELS OF ALL MANDESTINE THYMUS, SPLEEN, AND INTESTINE, THE LEVELS OF ALL MANDESTINE THE THYMUS, SPLEEN, AND INTESTINE, THE LEVELS OF ALL MANDESTINE EQUIVALENT.

INDUCTION: BY UV LIGHT.

INDUCTION: BY UV LIGHT.

DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1.

REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOWAL PROTEIN L5 AND A PUTATIVE C4-TYPE ZING FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MIDM4. IT IS ALSO ESSENTIAL FOR ITS UBIQUITIN LIGASE E3 ACTIVITY TOWARD P53 AND ARMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL LINE.
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 RANBP2-TYPE ZINC FINGER.
SIMILARITY: BELONGS TO THE MDM2 / MDM4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEPENDENT MANNER DISEASE: THE GENI
                                                                                                                                                                                                                            MGI:96952; Mdm2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATED IN RESPONSE TO IONIZING
                                                                                                                                                                                                                                                                                 S15349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED AT LOW-LEVEL THROUGHOUT EMBRYO DEVELOPMENT AND IN ADULT TISSUES. MDM2-P90 IS MUCH MORE ABUNDANT THAN MDM2-P76 IN TESTIS, BRAIN, HEART, AND KIDNEY, BUT IN THE THYMUS, SPLEEN, AND INTESTINE, THE LEVELS OF THE MDM2 PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 2 ISOFORMS; P76; ARE PRODUCED BY ALTERNATIVE ?
                                                                                                                                                                                                                                                     Q9UMT8; 1YCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INITIATION
                                                                                                                                                                                                                                                                          S15349.
                                                                                                                                                                                                                                                                                                                          AAB09030.
AAB09030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA41684.1;
AAA91167.1;
                                                                                                                                                                                                                                                                                                   AAB09031.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB09030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB09030.1;
AAB09030.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB09030.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENE
                                                                                                                                                   Znf_ring.
                                                                                                                                                                            Znf-RanBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR
                                                                                                                                                                                                                                                                                                                                                                                                             JOINED
JOINED
JOINED
JOINED
                                                                                                                                                                                                                                                                                                                JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
       FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN IS AMPLIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDM2-P90 (SHOWN HERE) AND MDM2-SPLICING AND ALSO BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
1. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RADIATION IN AN ATM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A MOUSE TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no
```

```
RESULT
MDM2_H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).

SIMILARITY SUBUNIT: BINDS P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA PROTEIN (RB), E1A-ASSOCIATED PROTEIN P300 AND THE EZF1 TRANSCRIPTION FACTOR (BY SIMILARITY).

PROTEIN (RB), E1A-ASSOCIATED PROTEIN P300 AND THE EZF1 TRANSCRIPTION FACTOR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR AND CYPOLASMIC. EXPRESSED PREDMINANTLY IN THE NUCLEOPLASM (BY SIMILARITY).

-!- DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND EZF1.

REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A DUTATIVE C4-TYPE ZINC FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH RNA WHETHER OR NOT ZINC IS PRESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MDM4. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                   -
                                                                                                                                                                                                CANCET Lett. 152:9-13(2000).

CIACCHE LETTON: INHIBITS P53- AND P73-MEDIATED CELL CYCLE ARREST AND APOPTOSIS BY BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN. FUNCTIONS AS AN UBIQUITIN LIGASE E3, IN THE PRESENCE OF E1 AND TOWARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND TARGETS IT FOR PROTEASOME-MEDIATED PROTEOLYSIS (BY SIMILARITY).

COPACTOR: ZINC IS REQUIRED FOR UBIQUITIN LIGASE E3 ACTIVITY (BY
                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                             canine and equine homologues proto-oncogene.";
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
0biquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-binding Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Argyle D.J.
                                                                                                                                                                                                                                                                                                                                                   Nasir L.,
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20218866;
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDM2_HORSE
P56951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; Ligarity Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                        caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                    sequence analysis and
                                                                                                                                                                                                                                                                                                                                                Burr P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
203
208
240
240
221
297
436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation
                                                                                                                                                                                                                                                                                                                                            PubMed=10754200;
D., McFarlane S.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligase; Ubiquitin cing; Alternative i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203
419
486
54543
                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
182
195
213
302
329
329
236
477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.
                                                                                                                                                                                                                                                                                                     and expression of the cDNAs of the mouse double minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S -> T (IN
D -> H (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RING-TYPE. NUCLEOLAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANBP2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER.
ARF BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGION I.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGION II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> H (IN REF. 1).
-> T (IN REF. 3).
4ABF489E92038DF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiation; Z
                                                                                                                                                                                                                                                                                                                                            Gault E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (P53-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                            Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n; Oncogene;
Zinc; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                   encoding 2 (mdm2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                      ZINC
ES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                 the
                                                                                         STI
                                                                                                                                                                                                                                     E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

۲,

```
RESULT MERCULT MERCULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00641; zf-RanBP; 1.

SMART; SM00184; RING; 1.

PROSITE; PS01358; ZF_RANBP2_1; 1.

PROSITE; PS50199; ZF_RANBP2_2; 1.

PROSITE; PS50089; ZF_RING_1; FAL

PROSITE; PS50089; ZF_RING_2; 1.
 Vogelstein B.;
"Amplification
sarcomas.";
                                                                                                                                                                                                                                                                                               MDM2_HUMAN
Q00987; Q13
Q9UMT8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2092 (Rel. 41, Last annotation update)
Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (P53-Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02279; MDM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                  Oliner J.D.,
                                                                 SEQUENCE FROM N.A. MEDLINE-92310576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                             MDM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITSELF (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 RANBP2-TYPE ZINC FINGER.
SIMILARITY: BELONGS TO THE MDM2 / MDM4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                         LLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UMT8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF121140;
                                                                                                                                                                                                                                                                                                                 Q13226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metal-
19
179
179
190
210
210
242
243
299
438
466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IPR003160; MDM2.
; IPR001876; Znf-R; IPR001841; Znf_r;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESSENTIAL FOR ITS
LF (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            æ
                                                  Kinzler
                                                                                                                                                                                                                                                                                                                 STANDARD; (013297; (
                  of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF28866.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligase;
                                               PubMed=1614537;
ler K.W., Meltzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
185
202
304
315
215
215
331
301
379
479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding.
                                                                                                                                      Chordata;
Primates;
                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Znf-RanBP.
Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITS UBIQUITIN
                                                                                                                                                                                                                                                                                                                 Q13298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubiquitin
              encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥
                                                  Meltzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB Pred. No. 58; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGION II.
ASP/GLU-RICH (ACIDIC).
RANBP2-TYPE.
RING-TYPE.
RUCLEDIAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
641E033D5C1DEC39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARF BINDING.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION SIGNAL NUCLEAR EXPORT SEQUENCE.
                                                                                                                                                                                                                                                                                                                PRT; 491
8; Q13299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGION
                                                                                                                                      Craniata; V
Catarrhini;
                ω
                                               P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugation; Oncogene;
              p53-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGASE E3
                                                                                                                                                                                                                                                                                                                                  491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                Q13300;
                                                                                                                                      Vertebrata; Euteleostomi; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                               George D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                      (P53-binding tein) (Hdm2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITY TOWARD
                                                                                                                                                                                                                                                                                                                 Q13301; Q9UGI3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 þ
                                                                                                                                                                                                                        protein
                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
```

```
MUTAGENESIS OF CYS-449.
MEDLINE-20190101; PubMed=1072:
Honda R., Yasuda H.;
"Activity of MDM2, a ubiquiting dependent on the RING finger of Oncogene 19:1473-1476(2000).
                       and p53."
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE-20065171; PubMed-10597303; Veldhoen N., Metcalfe S., Milner J.; "A novel exon within the mdm2 gene modulates translation initiation vitro and disrupts the p53-binding domain of mdm2 protein."; Oncogene 18:7026-7033(1999).
                                                                                                                                                                                                                                                                         Taubert H., Kappier M., Meye A., Bartel F., Schlott T., Lautenschlaeger C., Bache M., Schmidt H., Wuerl P., "A MboII polymorphism in exon 11 of thanan MDM2 gene conormal blood donors and in soft tissue sarcoma pattients: indication for an increased cancer susceptibility?"; Mutat. Res. 456:39-44(2000).
                                                                                                                                                                                                                                                                                                                                                                                Cancer
[8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE-95380270; PubMed-7651818;
MEDITINE-95380270; PubMed-7651818;
Zauberman A., Flusberg D., Haupt Y., E
"A functional p53-responsive intronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liang H., Atkins H., Abdel-Fattah R., Suaeyun R., "Genomic Organisation of the Human MIM2 Oncogene its Alternatively Spliced mRNA's.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (IS MEDLINE=20065171; Pubm Veldhoen N., Metcalfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sigalas I., Calvert A.H., Anderson J.J., Neal "Alternatively spliced mdm2 transcripts with domain sequences: transforming ability and fre
                                             MEDLINE=20187618; PubMed=10722742; Fang S., Jensen J.P., Ludwig R.L., Vousden "Mdm2 is a RING finger-dependent ubiquitin
                                                                                                                                                                                                              MUTAGENESIS OF CYS-40 MEDLINE~98111004; Pub Honda R., Tanaka H., "Oncoprotein MDM2 is
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97413643; pubMed=9270029;
Landers J.E., Cassel S.L., George D.L.;
"Translational enhancement of mdm2 oncogene
cells containing a stabilized wild-type p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer.";
Nat. Med.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Ovarian carcinoma; MEDLINE=96313107; PubMed=8705862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
[2]
                                                                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                                                                                                                                                                         MEDLINE=20542019; PubMed=11087894;
Taubert H., Kappler M., Meye A., B.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 301-481 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-9 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zauberman A., Flusherg D., Hara Ranctional p53-responsive the human mdm2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                    MUTAGENESIS
                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358:80-83(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 1-24 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A. (ISOFORMS
                        Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2:912-917(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                   420:25-27(1997).
OF.
                                                                                                                                                                                                                                                    OF CYS-464.
                                                                                                                                                                                                                                                                                                                                                                                          57:3562-3568(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 - 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
CYS-441 AND CYS-478
                       275:8945-8951(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM
                                                                                                                                                              PubMed=10723139
                                                                                                                                                                                                                                     PubMed=9450543;
                                                                                                                         a ubiquitin
ING finger do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23:2584-2592(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM MDM2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORM MDM2-ALPHA).
                                                                                                                                                                                                                þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
                                                                                                                                                                                                                           Yasuda
                                                                                                                                                                                                             ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A. (ISOFORM MDM2-A1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                            Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                         in ligase,
domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDM2-A;
                                                                                                                                                                                                             ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barak Y., promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ė
                                                                                                                         toward p53
the ligase
                                                                                                                                                                                                               E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ċ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eal D.E., Lunec J.;
th loss of p53 bind
frequent detection
                                               K.H., Weissman
protein ligase
                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                      expression protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oren
is co
                                                                                                                                                                                                               tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       en M.;
contained
                                                                                                                            ... ° ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lunec J.;
ind Relationship
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Έ).
                                                                                                                                                                                                               suppressor
                                                                                                                                     itself
                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                 occuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binding
ction in
                                                                                                                                                                                                                                                                                                     an
                                                A.M.;
for i
                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        within
                                                                                                                                      is
                                                 itself
                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĺη
```

between the Euro

ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a

and the

EMBL

outstation

no g

way

use

```
Transactivation domain.";

XL Science 274:948-953(1996).

C-1- FUNCTION: INHIBITS P53- AND P73-MEDIATED CELL CYCLE ARREST AND CI-1- FUNCTION: INHIBITS P53- AND P73-MEDIATED CELL CYCLE ARREST AND CREATED BY BINDING ITS TRANSCRIPTIONAL ACTIVATION DOMAIN.

CC FUNCTIONS AS AN UBLOUITIN LICASE B3, IN THE PRESENCE OF E1 AND E2, TOWARD P53 AND ITSELF. PERMITS THE NUCLEAR EXPORT OF P53 AND CC TARGETS IT FOR PROTEASOME-MEDIATED PROTEOLYSIS.

CC -1- COPACTOR: ZINC IS REQUIRED FOR UBLOUTIN LICASE E3 ACTIVITY.

CC -1- COPACTOR: ZINC IS REQUIRED FOR UBLOUTIN LICASE E3 ACTIVITY.

CC -1- SUBUNIT: BINDS P53, P73, ARF(P14), RIBOSOMAL PROTEIN L5 AND SPECIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA CREDITION FACTOR.

CC -1- SUBCIFICALLY TO RNA. CAN INTERACTS ALSO WITH RETINOBLASTOMA CREDITION FACTOR.

CC -1- COPACTOR: CRB), E1A-ASSOCIATED PROTEIN POOLASMIC. EXPRESSED CREDITION FACTOR.

CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. EXPRESSED CREDITS IN THE LOCALIZATION OF BOTH PROTEINS TO THE NUCLEOLUS. THE NUCLEOLAR LOCALIZATION OF BOTH PROTEINS TO THE NUCLEOLUS. THE NUCLEOLAR LOCALIZATION SIGNALS IN BOTH ARF(P14) AND MDM2 MAY BE NUCLEOLAR LOCALIZATION SIGNALS IN BOTH ARF(P14) AND MDM2 MAY BE
 MEDLINE=20079591; PubMed=10611322; Khosravi R., Maya R., Gottlieb T., Oren "Rapid ATM-dependent phosphorylation of in response to DNA damage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lohrum M.A.E., Ashcroft M., Kubbutat M.H.G., Vousder "Identification of a cryptic nucleolar-localization nat. Cell Biol. 2:179-181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharp D.A., Kratowicz S.A., Sank M.J., "Stabilization of the MDM2 oncoprotein structurally related MDMX protein.";
                               DEPENDENT MANNER.

IDESCASE: SEEMS TO BE AMPLIFIED IN CERTAIN TUMORS (INCLUDING SOFT TISSUE SARCOMAS, OSTEOSARCOMAS AND GLIOMAS). A HIGHER FREQUENCY C SPLICE VARIANTS LACKING P53 BINDING DOMAIN SEQUENCES WAS FOUND IN LATE-STAGE AND HIGH-GRADE OVARIAN AND BLADDER CARCINOMAS. FOUR OF THE SPLICE VARIANTS SHOW LOSS OF P53 BINDING.

I-MISCELLANEOUS: MDM2 RING FINGER MUTATIONS THAT FAILED TO UBIQUITINATE P53 IN VITRO DID NOT TARGET P53 FOR DEGRADATION WHEN EXPRESSED IN CELLS.

I-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

I-SIMILARITY: BELONGS TO THE MDM2 / MDM4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levine A.J., Pavleticn w.r., "Structure of the MDM2 oncoprotein bound "Structure Annain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in response to DN Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kussie P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=97081050; PubMed=8875929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION BY ATM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20173879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOLAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20076498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [15]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 274:38189-38196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: 8 ISC
A1, MDM2-B, MDM2-C, MDM2-C,
ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUIT
ARE OBSERVED IN A RANGE OF
                                                                                                                                                                                                                                                                                                 DOMAIN: REGION I IS SUFFICIENT FOR BINDING P53 AND INHIBITING ITS G1 ARREST AND APOPTOSIS FUNCTIONS. IT ALSO BINDS P73 AND E2F1.

REGION II CONTAINS MOST OF A CENTRAL ACIDIC REGION REQUIRED FOR INTERACTION WITH RIBOSOMAL PROTEIN L5 AND A PUTATIVE C4-TYPE ZINC FINGER. THE RING FINGER DOMAIN WHICH COORDINATES TWO MOLECULES OF ZINC INTERACTS SPECIFICALLY WITH MICH COORDINATES TWO MOLECULES OF RESENT AND MEDIATES THE HETERO-OLIGOMERIZATION WITH MICH. IT IS RESENT AND MEDIATES THE UBIQUITIN LIGASE E3 ACTIVITY TOWARD P53 AND SESSENTIAL FOR ITS UBIQUITIN LIGASE E3 ACTIVITY TOWARD P53 AND MEDIATES THE MEDIATION WITH MICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: BY DNA DAMAGE DOMAIN: REGION I IS SUFF
                                                                                                                                                                                                                                                                PTM: PHOSPHORYLATED IN RESPONSE TO IONIZING RADIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEINS
                                                                                                                                                                                                                                                                                       ITSELF
 SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorina S., Marechal V., Elenbaas B., Moreau
 entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. U.S.A. 96:14973-14977(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10707090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10608892;
 Ľ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UBIQUITOUS. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S: 8 ISOFORMS; MDM2
MDM2-D, MDM2-E AND
copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORMS
N CANCERS
 It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND MDM2-ALPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                George D.L.;
by interacti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interaction with the
 produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHOWN HERE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shiloh Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDM2-A,
BUT ABS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vousden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53 tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-A, -B,
ABSENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                en K.H.;
n signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Shkedy D.; p53 accumula
                                                                                                                  DEGRADATION WHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٦.,
                                                                                                                                                                     WAS FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ر.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDM2-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accumulation
                                                                                                                                                                                                                                                                  IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRODUCED
                                                                                                                                                                                                                                                                  ΑN
   collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDM2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND E2
                                                                                                                                                                                                                                                                  ATM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDM2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВУ
```

```
TYWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
YD56_SC
  망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; iPR003160; MDM2.
InterPro; iPR001895; Znf_ranBP.
InterPro; iPR001841; Znf_ring.
InterPro; iPR001841; 1.
InterPro; iPR001841; 1.
InterPro; iPR001841; 1.
InterPro; iPR001841; 1.
InterPro; iPR001841; 2f_RanBP; 1.
InterPro; iPR001958; Zf_RanBP; 1.
InterPro; iPR001958; Zf_RANBP2_1; 1.
InterPro; iPR001959; Zf_RANBP2_2; 1.
InterPro; iPR00195; Zf_RING_1; FALSE_NEG.
IPR0SITE; PS00089; Zf_RING_2; 1.
InterPro; iPR09195; IPR09195; INTERPRO; INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M92424; AAA60568.1; --
EMBL; Z12020; CAA78055.1; --
EMBL; U33199; AAA75514.1; --
EMBL; U33200; AAA75515.1; --
EMBL; U33201; AAA75516.1; --
EMBL; U33202; AAA75517.1; --
EMBL; U33203; AAA75518.1; --
EMBL; U33203; AAA75518.1; --
EMBL; U328935; AAA692837.1; --
EMBL; U28935; AAA62237.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                U1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
Hypothetical 59.0 kDa protein C6C3.06
SPAC6C3.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U39736; AAA82061.1; -. EMBL; AJ251943; CAB64448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q10310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
DOMAIN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                         or send an email to license@isb-sib.ch).
                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YD56
                                                                                                                                                                                                      Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      between
                                                                                                                                                                                                                                                              STRAIN=972;
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                   schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S24354; S24354.
1YCR; 19-NOV-97
164785; -.
                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC009893; AAH09893.1; -. U28935; AAA82237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit
and this si
                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA82237.1; -.
CAA93619.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rmatics Institute. There are no restrictions institutions as long as its content is in atement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGION I.
                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
in chromosome
                                                                noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                            There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene;
                                                                                          and
                                                                                                                                                             EMBL
                                                                                                                                                                                                                                              Walsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is
                                                                                                                                                                               מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                          for
                                                                                                                                                                               collaboration
                                                                                                                                                          outstation
                                                                                                                                                                                                                                              S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                       in no way
                                                                                                                                   on
                                                                                                                                   its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

QΥ

```
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;

"Prediction of the coding sequences of unidentified human genes. I'

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0121-KIAA0160) deduced by

The coding sequences of 40 new genes (KIAA0121-KIAA0121-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA012-KIAA0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGA3_HUMAN STANDARD; PRT; 723 AA. 09NZ52; Q9UJY3; Q15017; Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP-ribosylation factor binding protein GGA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 515 AA; 5
                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dell'Angelica E.C., Puertollano R., Mullins C., Agu
Vargas J.D., Hartnell L.M., Bonifacino J.S.,
"GGAs: a family of ADP ribosylation factor-binding
adaptors and associated with the Golgi complex.";
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE Bone marrow; MEDLINE 96127530; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boman A.L., Zhang C.-J., Zhu X., Kahn R.A.; "A family of ADP-ribosylation factor effectors that can alter transport through the trans-Golgi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ear-containing, ARF-binding protein GGA3 OR KIAA0154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (SHORT ISOFORM).
MEDLINE=20214818; PubMed=10749927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20211638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (LONG AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLK
                                                                                                                                                        by non-profit institutions as long
; AF219138;
; AF190864;
; AF219139; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLLKLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 11:1241-1255(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149:81-94(2000).
; AAF42848.1;
; AAF05709.1;
; AAF42849.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8590280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed-10747089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB Pred. No. 61; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B0466464840B3F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
.
                                                                                                                                                      There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Golgi-localized,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aguilar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE TRAFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                        restrictions on
tent is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n genes.
deduced
                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                     collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IV
by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

```
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPOL_NPVAC
P18131;
01-NOV-1990
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                           between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           MEDLINE-89073763; PubMed=3059678; Tomalski M.D., Wu J.G., Miller L.K.; "The location, sequence, transcription, baculovirus DNA polymerase gene."; Virology 167:591-600(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
EMBL; M20744;
EMBL; L22858;
                                                                                                                                                                                                    polyhedrosis virus.";
Virology 202:586-605(1994).
-i- CATALYTIC ACTIVITY: N deoxynucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD003686; HRS; 1.
ProDom; PD021457; G_adapt_C;
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                               MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J.,
"The complete DNA sequence of Auto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autographa californica nuclear
Viruses: dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00288; VHS; 1. PROSITE; PS50179; VHS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00790; VHS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR0011121; G_ad
InterPro; IPR002014; HRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D63876; BAA09926.1; ALT_INIT. InterPro; IPR001121; G_adapt_C.
                                                                                                                                                                       -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                 STRAIN=C6;
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 KLLAKLLK 183
                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLKLLK
                                                                                                                                                                                          (DNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 16, Created)
(Rel. 32, Last sequence update)
(Rel. 37, Last annotation updat
ase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
188
357
453
624
598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
 AAA46692.1; -.
AAA66695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Golgi
313
146
232
360
457
629
709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAMMA-ADAPTIN C-TERMINAL.
MISSING (IN SHORT ISOFORM).
; 4F80D6032239168C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-VAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL POLY-PRO. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-SER.
                                                                                                                                                                                                                                                 J., Lopez-Ferber M., Autographa californica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyhedrosis virus (AcMNPV).
stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled
NDS TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d coil; Alternative ARF1 (IN LONG ISOFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
85;
                                                                                          There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                          and regulation
                                                                                                                                                                                                     triphosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                   Possee R.D.;
nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing
                                                                                                                           a collaboration
                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                           no
on
                                                                                              way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPOL_NPVBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPOL_NEVEM STANDAM
DPOL_NEVEM STANDAM
P41712; 092430;
01-NOV-1995 (Rel. 32, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
15-DEC-1998 (Rel. 37, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                      "Sequence "Sequence nucleopolyhedrovirus.";
nucleopolyhedrovirus.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILINE-95133178; PubMed=7831799;
Chaeychomsri S., Ikeda M., Kobayashi M.;
Nucleotide sequence and transcriptional analysis of the DNA
polymerase gene of Bombyx mori nuclear polyhedrosis virus.";
Virology 206:435-447(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002064; DNA_pol_B. Pfam; PF00136; DNA_pol_B; 1. Pfam; PF03104; DNA_pol_B_exo; 1. PRINTS; PR00106; DNAFOLB. SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00116; DNA_POLYMERASE_B; 1. Transferase; DNA_directed DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bombyx mori nuclear polyhedrosis virus (BmNPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding;
PROSITE; PS00116; DNA_POLYMERASE_B; 1. Transferase; DNA-directed DNA polymerase; DNA-binding; Early protein. POLY-LYS. DOMAIN 724 727
                                                                  InterPro; IPR002064; DNA_pol_B.
pfam; pF001136; DNA_pol_B; 1.
pfam; pF031104; DNA_pol_B_exo; 1
pRINTS; PR00106; DNAPOLB.
                                                                                                                           EMBL; D16231; BAA03756.1; -. EMBL; L33180; AAC63738.1; -.
                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY
                                                                                                                                                                                                                                                                                                                                                                             Gomi S.,
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-T3
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569
                                                       SMART; SM00486; POLBC;
                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the genome of Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Majima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   946
830
984 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early protein.
724 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   960
830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114307
                                                                                                                                                                                                                                                                                                                                                                             Maeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                           s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ASP.
R -> W (IN REF. 1).
MW; 156ABB6BA1B45A21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB; Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                      noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; L
1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA replication,
                              DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                     diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                    collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                       n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

. .

В

ω

KLFLKLMK

```
SOSFIT
                                                                      RESULT
CAPG_ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 7
                     Matches
                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPG_ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 12
STAAU
                                                                                                                                                                                                                                                "Sequence analysis and molecular characterization of
for the biosynthesis of type 1 capsular polysaccharic
Staphylococcus aureus.",
J. Bacteriol. 176:7005-7016(1994).
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                        Protein capG CAPG.
                                                                                                 EMBL; U10927; AAA64646.1; -.
ThterPro; IPR001451; Hexapep_transf.
                                                                                                                                                                                                                                                                                                           MEDLINE=95050273;
                                                                     Transferase;
SEQUENCE 1
                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                   Lin W.S.,
                                                                                                                                                                                                                                                                                                                      STRAIN-M
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1280;
                                                                                         PROSITE; PS00101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 KLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLL 7
   \vdash
                                                                                                                                                                                                                  POLYSACCHARIDE.
SIMILARITY: BELONGS TO THE CYSE/LACA/LDXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAAU
  KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                    Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                   Cunneen
                                                                      e; Repeat.
172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  947
954
116
245
250
258
478
941
                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951
4 959
245
245
250
258
479
941
952
114418
   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          31, Created)
31, Last sequence up
40, Last annotation
                                                                                          HEXAPEP_TRANSFERASES;
                                                                                                                                                                                                                                                                                                    T., Lee C.Y
                                                                                                                                                                                                                                                                                                            PubMed=7961465;
                                                                       19451 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%;
100.0%
                                82
75
                                . 9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ASP.

A -> S (IN REF. 1).

H -> Y (IN REF. 1).

H -> Y (IN REF. 1).

V -> I (IN REF. 1).

TA -> AG (IN REF. 1).

S -> G (IN REF. 1).

N -> NDN (IN REF. 1).

N -> NDN (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB; Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                      1;
                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                        1608180D13A10EA4 CRC64;
                        Mismatches
                                29;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                               DB
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; L
1.1e+02;
                                                                                                                                                                                 There are no restrictions
                                                                                                                                                                                                                                                                                cerization of genes required polysaccharide in
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 986;
                                                                                                                                                                                                                                                    TYPE 1 CAPSULAR
                                         Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                        Indels
                                                                                                                                                               and
                                                                                                                                                                                             EMBL
                                                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                 for
                        0;
                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                               in no way
                        Gaps
                                                                                                                                                                                    on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                        0;
```

```
RESULTIFIED OF THE PROPERTY OF
  RRAC OCC OCC DIT DAC
                                                                                                                                                                                                                                                                                                                                                                     RESULT
SOM1_SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local s
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID DISULFID DISULFID
                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-UL-1999 (Rel. 38, Last annotation
Somatolactin 1 precursor (SL).
Sparus aurata (Gilthead sea bream).
                                                                                                                                                                                                                                                                                                                 SOM1_SPAAU
P54863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q919H4;

01-MAR-2002 (Rel. 41, Created)

01-MAR-2002 (Rel. 41, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequencing of Tetraodon miurus somatolactin."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Somatolactin precursor (SL).
Tetraodon miurus (Congo puffer).
Eukaryota, Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetraodontidae; Tetraodon.
                                                                       Acanthomorpha; Acanthopterygii;
Sparidae; Sparus.
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutenopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoide
                                                                                                                                                                                                                                                                                                                                                                        SPAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: PITUITARY GLAND.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETMU
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF253066; AAF64522.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rand-Weaver M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOML_TETMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::||||||
212 EILLKLLK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; S

1 21

22 229

D 26 36

D 87 203

D 220 228

D 143 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00266; SOMATOTROPIN_1; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑĄ;
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Мау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26125 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.98;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
(BY SIMILARITY.
(BY SIMILARITY.
(BY SIMILARITY.
(C10CCF295D28C447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                         231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

```
RESULT 15
SOM2_SPAAU
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; Glycoprotein; Signal.
SIGNAL 1 24 POT
CHANN 25 231 SON
DISULFID 29 39 BY
DISULFID 89 205 BY
DISULFID 222 230 BY
CARBOHYD 145 145 N-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Astola A., Pendon C., Ortiz M., Valdivia M.M.; "Cloning and expression of somatolactin, a pitt to growth hormone and prolactin from gilthead saurata.";
                                                                                       TISSUE-Pituitary;

Cavari B., Funkenstein B., Kawauchi H.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: PITUITARY GLAND.

-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoide Sparidae; Sparus.
NCBI_TaxID-8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                     Somatolactin 2 precursor (SL).
Sparus aurata (Gilthead sea bream)
                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                    P79894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00103; hormone; 1. PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L49205; AAA98734.1;
HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pituitary; MEDLINE=97114243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00266; SOMATOTROPIN_1; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: PITUITARY GLAND.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Comp. Endocrinol. 104:330-336(1996).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 EILLKLLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                     SPAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
SOMATCLACTIN 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF COLORDOWN (POTENTIAL CRC64;
W; 67A44E7D43E02504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                        Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     231
                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pituitary hormone related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seabream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparus
and
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
```

```
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).

CC or send an email to license@isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).

CC or send an email to license@isb-sib.ch/announce/CC or send an email to license.

CC or send an email to license@isb-sib.ch/announce/CC or send an email to license.

CC or send an email to license@isb-sib.ch/announce/CC or send an email to license.

CC or send an email to li
```

الحي

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein -
                                                                                                                                                                ĕ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
BB
                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length:
seq length:
  30
30
30
30
30
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw model
                                                                                                                                                            %
Query
Match
                                                                                                                                                                                                                                                   7:
8:
9:
110:
112:
115:
115:
  US-09-367-714A-29
35
1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 17, 2002, 12:44:20 ; Search time 73.61 Seconds (without alignments) 18.801 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                           sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
                                                                                                                                                                                                                                                                                                                                     sp_organelle:*
                                                                                                                                                                                                                                                                                                                                              sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                        sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                  sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                         sp_human: *
                                                                                                                                                                                                                                                                                                                                                                                  sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                             sp_bacteria:*
                                                                                                                                                                                                                                                                                       sp_vertebrate:*
                                                                                                                                                                                                                                                                                                        sp_rodent:*
                                                                                                                                                                                                                                                                                                                 sp_plant:*
                                                                                                                                                                                                                                                                                               sp_virus:*
                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000000000
 302
542
194
236
236
259
359
359
387
387
387
960
1211
60
66
                                                                                                                                                               DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapext 0.5
                                                                                                                        Q26784
Q91ZC1
Q91YF2
Q91086
Q96DS5
Q96DS3
Q96DS1
Q9R2T1
                                                                                                                                                               ij
                                                                                   Q948F3
Q92HH2
Q88829
Q9QWF8
                                                        Q9HK94
Q9CZ65
Q9QWF9
                                                 Q91GJ3
                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562222
O26784 trypanosoma
O91scl salem virus
O91yf2 mus musculu
O948f3 oryza sativ
O948f3 oryza sativ
O92hh2 rickettsla
O88829 mus musculu
O99wf6 mus musculu
O99wf6 mus musculu
O99wf9 mus musculu
O99wf9 mus musculu
O99wf9 mus musculu
O910f3 epiphyas po
O910f6 meleagris g
O96ds1 homo sapien
O96ds1 homo sapien
O96ds1 homo sapien
O96ds1 homo sapien
                                                                                                                                                              Description
```

Ű.	_	~	٠	-	_	•	~	•	ψ,	Ψ.	•	_			_	_	_		<u>.</u>	٥.	-	_			_	_	_	_
30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
				•	85.7	•	•	85.7	•	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	5	85.7	ū	85.7	5	5	ပာ	5	S	5	5
644	633	633	631	586	586	489	487	487	418	396	325	321	282	243	237	217	195	191	166	162	159	137	135	130	110	110	110	110
11	4	4	4	11	4	11	6	σ	10	4	13	17	16	4	4	10	4	17	16	œ	4	1	ഗ	4	2	N	N	N
Q9JIM7	Q9Н952	Q9NRK5	Q9NRN1	Q9JIQ6	Q9NRU3	Q91XK7	Q95KN5	Q9GMZ6	Q9LDC5	Q9NXT4	Q9PVL2	058243	Q9ZLZ4	Q9H4C5	Q96LK7	Q942V5	Q96DS4	Q97W19	99469	Q950Q3	096DS0	Q9DBL5	Q95WZ4	Q9H4C3	Q44792	Q9RZZ6	Q9S047	Q9S089
Q9jim7 mus musculu	homo	Q9nrk5 homo sapien	Q9nrn1 homo sapien	mus	Q9nru3 homo sapien	Q91xk7 mus musculu	Q95kn5 canis famil	canis	Q9ldc5 oryza sativ	~	Q9pvl2 gallus gall		Q9z1z4 helicobacte		homo s	ory	S OWO	9	10	Q950q3 spizellomyc	Q96ds0 homo sapien	Q9dbl5 mus musculu	Q95wz4 ixodes scap	Q9h4c3 homo sapien		Q9rzz6 borrelia bu	Q9s047 borrelia bu	Q9s089 borrelia bu

 $\begin{array}{c} 117 \\ 127 \\$

ALIGNMENTS

PRT;

302

A

```
RESULT
10 267 84
AC QQ
DT DT 0
DT 0
DT 0
OC T 0
OC T 0
OC T T 0
OC
      RESULT
Q91ZC1
ID Q
AC Q0
DT 00
DT 00
DT 00
                                                                                                                                                                                                                                                                                                  망
                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M87
NON_TER
SEQUENCE
Q9IZC1;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q26784; PRELIMINARY;
Q26784; Ol-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC_2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95140053; PubMed=7838181;
Woodward R., Carden M.J., Gull K.;
"Molecular characterisation of a novel, repetitive protein of the paraflagellar rod in Trypanosoma brucei.";
Mol. Biochem. Parasitol. 67:31-39(1994).
EMBL; M87318; AAC37211.1; -...
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida;
NCBI_TaxID-5691;
                                                                                                                                     Q9IZC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRNA SEQUENCE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               |||||:||
21 KLLLKVLK 28
                                                                                                                                                                                                                                                                                                                                                               1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.48;
87.5%;
          15,
15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB Pred. No. 98; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B3CA5AB868E877CC CRC64;
                                                                                                                                         542
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosomatidae; Trypanosoma
                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 302
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
RESULT
OPINE
AC
OPINE
RESULT Q948F3 ID Q948F3 OC EE COC SI OC NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                             01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
PUTATIVE RIBONUCLEOTIDE FOTOLOGY 1
OSJNBA0049012.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renshaw R.W., Glaser A.L., Van Campen H., Weiland F., Dubovi E.J.;
"Identification and phylogenetic comparison of salem virus, a novel
paramyxovirus of horses.";
Virology 270.417-429(2000).
EMBL; AF237881; AAF63741.1; -
InterPro; IPR002021; Paramyx_ncap.
Pfam; PF00973; Paramyx_ncap; 1.
SEQUENCE 542 AA; 60717 MW; F057ECF483F1F7D9 CRC64;
                                                                                                                                                                                                                                Q948F3;
Q948F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL; Y18023; CAC79655.1; -. SEQUENCE 194 AA; 22205 MW; E68780E30BFE84EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91YF2;
Q91YF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=120499;
                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20255542; PubMed=10793001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paramyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salem virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shuichi
    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHASE PROTEIN. SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLLKLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                     KFLLKLLK 182
                                                                                                                                                                                                                                                                                                                                                                                                                KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paramyxovirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%;

    Created)
    Last sequence update)
    Last annotation update)
    REDUCTASE (FRAGMENT).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB
Pred. No. 1.6e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paramyxovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
                                               Embryophyta; Tracl
a; Poales; Poaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae;
                                                                       Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

```
RESULT
Q92HH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                     Qy
                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q92HH2;
Q92HH2;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Protec
Rickettsiaceae;
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spiegel L., Nascimento L., de la Bastide M., Kirchoff K., Prestv. King L., Vil M.D., Baker J., Zutavern T., Santos L., Miller B., Kuit K., Cunnius D.M., Balija V., Saha R., Bahret A., Bell M., Yang C., Palmer L., O'Shaughnessy A., Dedhia N., McCombie W.R.; "Genomic Sequence for Oryza sativa, Nipponbare strain, clone OSJNBa0049012, from chromosome 2, complete sequence."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                      01-NOV-1998 (TremBLrel.
01-NOV-1998 (TremBLrel.
01-JUN-2001 (TremBLrel.
GM3 SYNTHASE (EC 2.4.99.
                                                                                                                                                                                                                                                                                      EMBL;
           Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                             SIAT9
                                                                                                                                                                                                                                                                   Hypothetical protein; Complete SEQUENCE 296 AA; 33899 MW;
                                                                                                                                                                                                                                                                                                                              Ogata H., Audic S.,
Samson D., Roux V.,
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia conorii.
Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC069158; AAK98710.1; NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NIPPONBARE;
                                                                                                 088829;
                                                                                                             088829
                                                                                                                                                                                                                                                                                       Science 293:2093-2098(2001)
EMBL; AE008635; AAL03337.1;
                                                                                                                                                                                                                                                                                                                       Raoult D.;
                                                                                                                                                                                                                                                                                                                                  MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weisse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             Mechanisms of evolution
                                                                                                                                                                    287
                                                                                                                                                                                      1 KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLLLKLLQ
                                                                                                                                                                    KILLKILK
                                                                                                                                                                                                            Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA;
                                                                                                                                                                                                           88.6%;
nilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN RC0799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                                                                    294
                                                                                                                                                                                       8
            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26749 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.6%;
87.5%;
                                                       08,
08,
17,
.9).
                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                 Last sequence update)
Last annotation update)
                                                                                       Created)
                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                             Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                             Score 31; DB Pred. No. 1.56 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 10;
Pred. No. 1.2e+02;
            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D29916BA145DC49A CRC64;
                                                                                                                                                                                                                                                                    proteome.
381A649E1DDBAB5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                   iffren P., Fournier P.-E.,
Weissenbach J., Claverie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296
                                                                                                               359
                                                                                                                                                                                                                                                                                                               conorii
                                                                                                                                                                                                                        DB 16;
1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                               R. prowazekii.";
                                                                                                                                                                                                                                      296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preston
                                                                                                                                                                                                                                                                                                                                                Barbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                0
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
 Query Match
Best Local S
Matches 7
                                                                   KONO M., Takashima S., Liu H., Inoue M., Kojima N., Yo
Hamamoto T., Tsuji S.;
Molecular cloning and characterization of fifth type
galactoside alpha-2, 3-sialyltransferase (ST3Gal V; GM.
Biochem. Biophys. Res. Commun. 253:170-175(1998).
EMBL, Y15003; CAA75236.1; -.
RMGD; MGI:133963; Siat9.
RINTERPOOF CARCOLUMN CONTROLOGICAL STATES (STATES).
R Pfam; PF00777; Glyco_transf_29.
Fransferase; Glyco_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                       Q9QWF8;
Q9QWF8;
Q9QWF8;
Q1-MAY-2000 (TrEMBLrel. 13, Createg)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TACTOSYLCERAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N. F
STRAIN-C57BL6J;
                                                                                                                                                                                                                                                     ACL:
SIAT9 OR STJun...
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukumoto S., Miyazaki H., Urano T., Furukawa K.; "Expression cloning of mouse cDNA of CMP-NeuAc: lactosylceramide alpha2, 3salyltransferase (cM3 synthase), the enzyme that initiates the synthesis of gangliosides).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (\overline{SEP}-1998) {2}
                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB-C
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Q9QWF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Kapitonov D., Yu R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                   STRAIN=ICR; TISSUE=BRAIN;
MEDLINE=99092398; PubMed=9875239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Combinatorial PCR in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mouse GM3 Synthase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB018048; BAA33491.1; -.; AB013302; BAA76467.1; -.; AF119416; AAF66147.1; -. MGI:1339963; Siat9.
                                                                                                                                                                                                                                                                                                                                                                                                                                             KFLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR001675; Glyco_transf_29
PF00777; Glyco_transf_29; 1.
ferase; Glycosyltransferase.
NCE 359 AA; 41245 MW; 38D81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
7; Conserv
  Similarity 7; Conserv
                                                               359
  Conservative
                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
J; TISSUE=BRAIN;
                                                               A
A
                                                              41235 MW;
              88.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ťo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ
Score 31; DB Pred. No. 1.8e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31;
Pred. No.
                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                              8E3C734CD1899E3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38D81D0B8CFC4961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cloning: cloning
              1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
                          DB 11;
                                                                                                                                                                                       Kojima N., Young-Choon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8e+02;
                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                        Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 359;
                                                                                                                                                                 type of beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of GM3 synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
  Indels
                                                                                                                                                   GM3 synthase).";
                                                                                                                                                                                                                                                                                                                .9)
  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
 0;
```

```
RESULT
Q9HK04
ID W09
AC Q9
AC Q9
DT DT 0:
CO Q9
ON T 0:
CO
        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HK94;
01-MAR-2001
01-MAR-2001
01-JUN-2001
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9CZ65;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIALLITRANSFERASE 9 (CMP-NEUAC:LACTOSYLCERAMIDE ALPHA-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 407:508-513(2000).

Nature 407:508-513(2000).

EMBL; AL445065; CAC11845.1; -.

InterPro; IPR001296; Glycos_transf_1.

Pfam; PF00534; Glycos_transf_1; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 384 AA; 44734 MW; BEC8D05CF0237E40 CRC64;
                                                                                                                                                                                                              Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAO/טי.
Thermoplasma acidophilum.
Thermoplasmales; Thermoplasmales; Thermoplasmaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HK94
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIALYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9CZ65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DSM 1728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TA0707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20479972; PubMed-11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 KLLMKILK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFLLKLLK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 16,
(TrEMBLrel. 16,
(TrEMBLrel. 17,
L PROTEIN TA0707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB Pred. No. 1.9e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                 Fukuda S.,
Yamanaka I.,
Saito R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

```
RESULT Q91GJ3
ID Q5
AC Q6
DT 0:
DT 0
DT 0
DE D D
GN D
GN E
                                                                                                                                                                                                                                                                     Вþ
                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QWF9;
Q9QWF9;
Q9QWF9;
Q1-MAY-2000 (TrEMBLrel. 13, Createq)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                Q91GJ3;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-99092630, FLUCTOR MODELINE-99092630, FLUCTOR M., KOOD M., Takashima S., Liu H., Inoue M., Kojima w., Kono M., Takashima S., Liu H., Inoue M., Kojima w., Hamamoto T., Tsuji S.;
"Molecular cloning and characterization of fifth ty:
"Molec
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y15003; CAA75235.1; --
MGD; MGI:1339963; Slat9.
InterPro; IPR001675; Glyco_transf_29.
Pfam; PF00777; Glyco_transf_29; 1.
Transferase; Glycosyltransferase.
SEQUENCE 387 AA; 44562 MW; CBD1ECDF5E390ACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                      Q91GJ3
                         DNAPOL
                                              DNAPOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun.
EMBL; Y15003; CAA75235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ICR; TISSUE=BRAIN; MEDLINE=99092398; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QWF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AK012961; BAB28871.1; -.
MGD; MGI:1339963; Siat9.
InterPro; IPR001675; Glyco_transf_29.
Pfam; PF00777; Glyco_transf_29; 1.
SEQUENCE 387 AA; 44572 MW; 7D358298034CDD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasa K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                   368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                               <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLK
                                                                                                                                                                                                                                                                                                             KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 P.,
                                                                                                                                                                                                                                                                   KFLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFLLKLLK
                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
postvittana
                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                   375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
nucleopolyhedrovirus
                                                                                                                                                                                                                                                                                                                                                                              88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                              . 5%;
                                                                19,
19,
                                                              Last
Last
                                                                                                                                                                                                                                                                                                                                                  Score 31; DB
Pred. No. 1.9e
0; Mismatches
                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7D358298034CDD96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                            sequence update)
annotation update)
                                                                                                                                                    960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                           DB 11;
1.9e+02;
                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                              Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type of beta-
v; GM3 synthase).";
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young-Choon
                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

```
Ъ
                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQ RTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
                                         Matches
                                                    Query Match
Best Local
                                                                                           PRINTS; PRO0390; PHPHLIPASEC.
ProDom; PD001202; PI_PIC_Y; 1.
SMART; SM00239; C2; 1.
SMART; SM00148; PLCXC; 1.
SMART; SM00149; PLCYC; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50007; PIPIC_X_DOMAIN; 1
PROSITE; PS50008; PIPIC_X_DOMAIN; 1
PROSITE; PS50008; PIPIC_X_DOMAIN; 1
SEQUENCE 1211 AA; 139061 MW; 4E
                                                                                                                                                                                                                                                                   EMBL; U49431; AAC60011.1; ... HSSP; P10688; 1QAS.
                                                                                                                                                                                             Pfam; PF00168; C2; 1.
Pfam; PF00388; PI-PLC-X; 1.
Pfam; PF00387; PI-PLC-Y; 1.
                                                                                                                                                                                                                                                                                           erythrocytes.
Biochem. J. 3
                                                                                                                                                                                                                                                                                                                  and beta gamma-subunit-stimulated
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96257751; PubMed=8687401;
                                                                                                                                                                                                                                                                                                                                                                                       Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Meleagr:
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TIEMBLIEL 01, 01-NOV-1996 (TIEMBLIEL 01, 01-JUN-2001 (TIEMBLIEL 17, PHOSPHOLIPASE C BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91086;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleopolyhedrovirus genome.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY043265; AAK85622.1;
SEQUENCE 960 AA; 111520 MW; OCBBABE2E0F5B540 CRC64;
                                                                                                                                                                                                                           InterPro; IPR000909;
InterPro; IPR001711;
                                                                                                                                                                                                                                                 InterPro; IPR000008; C2.
InterPro; IPR001192; PI_PLC.
                                                                                                                                                                                                                                                                                                                            "Molecular cloning, expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91086
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The
 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyink O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=70600;
                    1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V.K.;
KLFLKLLK 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLLLELLK
                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 87. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
Dellow R
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.A.,
                                                                                                                                                                                                                                                                                                                            n A., Boyer J.L., expression and re
                                                                                                                                                                                                                           PI_PLC_X.
                                                      88
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen
                                                    . 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA stage;
                                        Score 31; DB
Pred. No. 5.26
0; Mismatches
                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB Pred. No. 4.3e.
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epiphyas
                                                                                           1.
1.
4E96A10C6AFD6B5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caradoc-Davies K.M.B.,
                                                                                                                                                                                                                                                                                                               L., Nicholas R.A., Harden 1 d regulatory activity of G phospholipase C-beta from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
. 4.3e+02;
. ~ 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baculoviridae;
                                                    DB 13;
5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          postvittana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                         Meleagrididae; Meleagris
                                                             Length 1211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 960;
                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drake
                                                                                                                                                                                                                                                                                                                n T.K.;
G alpha
Dm avian
                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>۳</u>
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                            11-
                                       0;
```

```
Q96DS5
ID Q9
AC Q98
AC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
Q96DS3
ID
Q9
DT
Q9
DT
Q1
DT
Q
RESULT
Q96DS1
ID QS
AC QS
DT 01
DT 01
DT 01
DE ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96DS5 PRELIMINARY;
Q96DS5;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-RHABDOW/SSARCOMA TUMOR;
Bartel F., Taylor A.C., Taubert H., Harris L.C.;
Where I mdm2 splice variants identified in pediatric rhab tumors and cell lines.";
Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF385322; AAL13242.1;
EMBL; AF385322; AAL13242.1;
SEQUENCE 60 AA; 6652 MW; BCC2CC61C4CC98A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDM2.
Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
'`rvota; Primates;
Q96DS1 PRELIMINARY; PRT; Q96DS1; Q96DS1; C1DEC-2001 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-RHABDOMYOSARCOMA TUMOR;
Bartel F., Taylor A.C., Taubert H., Harris L.C.;
"Novel mdm2 splice variants identified in pediat:
tumors and cell lines.";
submitted (MAY-2001) to the EMBL/GenBank/DDBJ da
EMBL, AF38534; AAL13244.1;
SEQUENCE 66 AA; 7396 MW; E3B3F3C385D4A8A5 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
01-DEC-2001 (TremBLrel.
MDM2 VARIANT FB28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDM2 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96DS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96DS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                             IIIIIIII
LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FB25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%; >cc
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB Pred. No. 65; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E3B3F3C385D4A8A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                    sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pediatric rhabdomyosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pediatric rhabdomyosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
Query Match
Best Local Similarity
""+"hes 7; Conserv
Search completed:
Job time: 296 sec
                                                            밁
                                                                                  Š
                                                                                                                                                                        TISSUE-RHABDOMYOSARCOMA TUMOR;
Bartel F., Taylor A.C., Taubert H., Harris L.C.;
"Novel mdm2 splice variants identified in pediatric rhab
tumors and cell lines.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF385326; AAL13246.1;
SEQUENCE 95 AA; 10622 MW; 00052F95211E3612 CRC64;
                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=9606; [1]
                                                            33
                                                                                  2 LLLKLLK 8
                                                            LLLKLLK
                                                                                                            Conservative
           June
                                                            39
           17,
                                                                                                                        85.7%;
100.0%;
            2002,
            12:44:21
                                                                                                            0
                                                                                                                        Score 30;
Pred. No.
                                                                                                            Mismatches
                                                                                                                        89
80
                                                                                                                                                                                                                      p.L.C.;
pediatric rhabdomyosarcoma
                                                                                                                                    4;
                                                                                                            0;
                                                                                                                                    Length 95;
                                                                                                              Indels
                                                                                                           0;
                                                                                                            Gaps
```

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq
       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
6: /cgn2_6/ptodata/2/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
     BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-367-714A-29
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 17, 2002, 12:42:04; Search time 34.71 Seconds (without alignments) 5.630 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231628 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length DB
     24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapext 0.5
US-09-334-601-4
US-07-725-331-9
PCT-US91-05047-90
US-08-248-839C-47
US-08-248-839C-47
US-08-248-500A-5
US-08-390-546-5
US-08-390-546-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-5
US-08-390-515A-3
US-08-390-479A-3
US-08-390-479A-3
US-08-390-515A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231628
                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
   sequence
sequence
sequence
sequence
sequence
sequence
sequence
sequence
sequence
                                                                                                                                                                         Sequence
Sequence
Sequence
4 Appli
9 Appli
9 Appli
13 Appli
4 Appli
4 Appli
5 Appli
6 Appli
7 Appli
8 Appli
9 App
   COMPUTER: IBM PC compatible
```

RESULT 2 US-07-725-331- Sequence 9, Patent NO. 15 GENERAL INIT TITLE OF TITLE OF TITLE OF CORRESPON ADDRESS AD	Query Ma Best Loc Matches	RESULT 1 US-09-334-601 Sequence 4, Patent NO. 6 GENERAL INFE APPLICANT: APPLICANT: TITLE OF IN FILE REFERE CURRENT APP CURRENT APP CURRENT APP CURRENT FI NUMBER OF 5 SOFTWARE: E SOFTWARE: PRT TYPE: PRT ORGANISM: US-09-334-601	22 23 23 24 24 24 25 26 26 27 26 27 26 27 26 27 27 28 28 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20
JYS KFLLKLLK 402 LT 2 quence 9, Application tent No. 5294605 ENERAL INFORMATION: APPLICANT: Hought APPLICANT: Hought APPLICANT: HOUGH APPLICANT: HOUGH APPLICANT: Blonde TITLE OF INVENTION UNMBER OF SEQUENCE CORRESPONDENCE ADD CORRESPONDENCE ADD CORRESPE: Dres ADDRESSEE: & MI STREET: 180 No. CITY: Chicago CITY: Chicago CITY: USA ZIP: GOO1 COUNTRY: USA ZIP: GOO1 COUNTRY: GAO3 ZIP: GOO1 COUNTRY: GAO3 ZIP:	Simi Simi 7;	-601-4 -601-4 NO. 6280989 NO. 6280989 NO. 6280989 ANT: KAPITIONV: ANT: YU, ROBERT OF INVENTION: N EFFRENCE: VCUIP T APPLICATION N TT FILING DATE: COF SEQ ID NOS: RE: PATENTIN VE H: 414 PRT ISM: MUTINAE 96 -601-4	222222222222222222222222222222222222222
1Catio 1Catio 101 101 101 101 101 101 101 10	arity onserva 8	1 1.4-601-4 . No. 6280989 . No. 6280989 . CANT: Kaphtonov. CANT: Kaphtonov. Dm CCANT: Kry. Robert OF INVENTION: NOVE REFERENCE: VCUIP-6 NOT APPLICATION NUMB NOT FILING DATE: 199 R OF SEQ ID NOS: 94 ARE: Patentin Ver. TH: 414 :: PRT NISM: Murinae gen.	888888888888888888888 NNNNNNNNNNNNNNNN
on US/ en, Ri lle, Ri lle, Ri : Ang : Ang : Ang : Ang S: 68 S: 68 S: 52946	88. 87. tive	s 29EFis	111111111111111111111111111111111111
5/077253 Richard Sylvie mphiphil nalogues 58 Goldsm w 4605th S	, A. O. O.	· 0 0 · 0 · 0	U 4 4 4 0 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
n US/07725331 n, Richard le, Sylvie Amphiphilic Peptide Compositions Analogues Thereof : 68 : 68 ler, Goldsmith, Sutker, Shore, namow 5294605th Stetson ORM: ORM: ORM:	Score 31; DB 4; Length Pred. No. 2.1e+02; O; Mismatches 1; Inde	9334601 1 1 1ALYLTRANSFERASES US/09/334,601 6-17	US-08-465-325-138 US-09-115-737-138 US-07-725-331-1 US-08-569-188-8 PCT-US94-07019-8 US-07-725-331-4 US-08-569-188-1 US-08-569-188-11 US-08-569-188-11 US-08-569-188-12 US-08-569-188-12 US-08-569-188-12 US-08-569-188-13 PCT-US94-07019-1 PCT-US94-07019-1 PCT-US94-07019-10 PCT-US94-07019-11 ALIGNMENTS
and d	414; els 0;		Sequence
	Gaps		138, App 138, Appli 1, Appli 2, Appli 11, Appli 12, Appli 12, Appli 13, Appli 14, Appli 17, Appli 18, Appli 19, Appli 11, Appli

OPERATING SYSTEM: SOFTWARE: Patentl

PC-DOS/MS-DOS

Release #1.24

```
Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-07-725-331-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US91-05047-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 3126165460 INFORMATION FOR SEQ ID NO:
                                                             SOFTWARE: Patentin Release CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USS FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION DATA: US 07/:
APPLICATION NUMBER: US 07/:
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/554,422
APPLICATION NUMBER: US 07/554,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-JUL-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Houghten, Richard APPLICANT: Blondelle, Sylvie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dressler, Goldsmith, Sutker, Shore ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                    NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLLXKLLK 9
                                                                                                                                                                                                                                                                                                  60601
                                                                                                                                                                                                                                                                                                    ASD
                                                    Gamson, Edward P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 amino acids
                                                                                                                                                                                                                                                                                                                                                                 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is Met or methionine sulfoxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                     US 07/554,422
                                                                                                                                                                          PCT/US91/05047
                                    29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30;
Pred. No.
                   421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-944-133-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US91-05047-9
; TOPOLOGY: 1; MOLECULE TYPE: US-08-944-133-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08944133 Patent No. 5789542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 31Zb10700.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                  TELEFAX: 504 346-8049 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: At
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/789,077
FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                             FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 06-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 70821-2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P. O. Box CITY: Baton Rouge
                                                LENGTH: 21 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KLLXKLLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: John H. Runnels
P. O. Box 2471
                                                                                                                                    504 346-8049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is Met or methionine sulfoxide.
                                                                                                                                                                                                                                                                     us/08/232,525
                                                                                                                                                                                                                                                                                                    US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                    US/08/944,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                      13:
                                                                                                                                                                                    Atty File No. 5789542 9301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

0

.0

```
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                     RESULT 6
US-07-903-103-4
                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-248-839C-47
                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: Protein US-08-248-839C-47
           GENERAL INFORMATION:
APPLICANT: VOGELSTEIN, BERT
APPLICANT: KINZLER, KENNETH
TITLE OF INVENTION: AMPLIFICA
TITLE OF INVENTION: HUMAN TUM
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                       Sequence 4, Application US/07903103 Patent No. 5411860
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 47, Application US/08248839C Patent No. 5843702
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: McConnell, David
APPLICANT: Devine, Kevin
APPLICANT: O'Kane, Charles
TITLE OF INVENTION: A Gene Expression System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 3614
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 25-MAY-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                49 KIVLKLLK 56
                                                                                                                                                                                                                                                           Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KLALKLLK 9
                                                                                                                                                                                                                             1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: No. 58437020 No. 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%;
87.5%;
                                                                                                                                                                                                                                                                          85.7%;
75.0%;
                                           AMPLIFICATION OF HUMAN MDM2 GENE IN
                            HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/248,839C
                                                                                                                                                                                                                                                                                                                                                                                                                                               47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3614.214-US
                                                                                                                                                                                                                                                                        Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5843702disk of No. 5843702th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                     Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
```

```
; MOLECULE TYPE: protein US-07-903-103-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-044-619A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Watches 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08044619A Patent No. 5420263
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: THE JOHNS
APPLICANT: 720 RUTLA
TITLE OF INVENTION:
TITLE OF INVENTION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,103
FILING DATE: 23-JUN-1992
                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,619A
FILING DATE: 07-APR-1993
                                                                                                                                                                               COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 07-APR-1992
ATTORNEY, TAGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMI
                                                                                                                                                                                                                                                                      ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT STREET: 1001 G ST., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1001 G ST
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20001-4597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
                                                                                                                                                                                                                                                         D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1001 G ST.,
                                                                                                                                                                                                                                                                                                                                                                                THE JOHNS HOPKINS UNIVERSITY
720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
VENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANNER, BIRCH, MCKIE AND BECKETT
                                                                                                                                                                                                                                                                                                                                                                 HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/867.840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/903,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01107.40148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; L., 3. 3.6e+02; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

0;

밁

```
뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-044-619A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-283-911-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08283911 Patent No. 5519118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                APPLICATION NUMBER: US 0:
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 23-JUN-1992
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                              SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VOGELSTEIN, BERT APPLICANT: KINZLER, KENNETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                LENGTH:
                                                                          TELEFAX: 202-508-9295
TELEX: 197430 BBMB UT
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/283,911 FILING DATE:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/867.840 FILING DATE: 07-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20001-4597
            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: BANNER, BIRCH, MCKIE AND BECKETT 1001 G ST., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%;
                                                                                                                                                                                                                                    US 07/867.840
                                                                                                                                                                                                                                                                    us 07/903,103
                                                                                                                                                                32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,141
                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  b; Score 30; DB
b; Pred. No. 3.6
0; Mismatches
                                                                                                                                                01107.40148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01107.40148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

RESULT 10 US-08-390-546-5

Sequence 5, Applic Patent No. 5606044

Application US/08390546

0

GENERAL INFORMATION:
APPLICANT: BURREL

BURRELL, MARILEE HILL, DAVID E.

```
밁
                                       Query Match
Best Local Similarity
Trahas 7; Conserv
                                                                                                                        ; MOLECULE TYPE: US-08-245-500A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
"hes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-245-500A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-283-911-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Patent No.
                                                                                                                                                                                         TELEX: 197430 BBMB UT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1001
CTTY: WASHINGTON
33 LLLKLLK 39
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 LLLKLLK 39
                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                          2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20001
                                                                                                                                                               amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08245500A 5550023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001 G STREET, N.W.
                                                                                                                                                                                                                                     202-508-9299
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOGELSTEIN, BERT
                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINZLER, KENNETH W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BURRELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BANNER,
                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LL, MARILEE
DAVID E.
                                                 85.7%; Score 30;
100.0%; Pred. No.
Live 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 30;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIRCH, MCKIE AND BECKETT
                                                                                                                                                                                                                                                                                                                                                         US/08/245,500A
                                                                                                                                                                                                                                                                                       32,141
                                                                                                                                                                                                                                                                            01107.42798
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; I
. 3.6e+02;
                                                                              DB 1;
                                                                 3.6e+02
                                                                            Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 489
                                                    Indels
                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

```
Query Mätch
Best Logal Similarity
"~+~hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            US-08-390-479A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: US-08-390+546-5
                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08390479A Patent No. 5618921
                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 07-APR-1993
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT STREET: 1001 G STREET, NOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                            APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
                                                                                                                                                                                                                                                                                                                             APPLICANT:
               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                APPLICANT: VOGELSTEIN, BERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                              STATE: D.C
                                                                                                                              COUNTRY:
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LLLKLLK 8
                                                                                                                 20001
                                                                                                                                                              WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.C.
                                                                                                                                                                            E: BANNER & WITCOFF, LTD
1001 G STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 amino acids
                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                            BURRELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VOGELSTEIN, BERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINZLER, KENNETH W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                              AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                               MARILEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%; Score 30;
100.0%; Pred. No.
Live 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/390,546
US/08/390,479A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01107.42798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
TOPOLOGY: 1
MOLECULE TYPE:
```

밁 QΥ

```
Query Match
Best Local Similarity
Trines 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-390-479A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-557-393-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Approximately No. 5702903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                 TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                 NAME: KACAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  APPLICATION NUMBER: US 0
FILING DATE: 18-MAY-1994
AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                  SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KINZLER, KENNETH W. APPLICANT: VOGELSTEIN, BERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LLLKLLK 8
|||||||
33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1001 G ST
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-500 BBMB UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT STREET: 1001 G STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08557393
                    489 amino acids
                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 202-508-9100
202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BURRELL, MARILEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAVID E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                        US 08/245,500
                                                                                                                                                                                                                                                                                    us/08/557,393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01107.48992
                                                                                                                                      01107.42798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

0;

US-08-557-393-5

```
RESULT 14
US-08-390-517A-5
                                                                                                                             В
                                                                                                                                                                                                                                                        US-08-390-516C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
"hehes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-390-516C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                          Sequence 5, Application US/08390517A Patent No. 5736338 GENERAL INFORMATION:
                                                                                                                                                                                    Matches
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5708136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08390516C Patent No. 5708136
                                                                                                                                                                                                                                                                                                      TELEX: 197430 BBMB UT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 489 amino acid
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                           NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE, DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AMPLIFICATION HUMAN TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                            33 LLLKLLK 39
                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                  Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0:
FILING DATE: 07-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: WASHINGTON
                                                                                                                                                       2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20001
                                                                                                                                                                                                                                                                                             amino acid
BURRELL, MARILEE HILL, DAVID E.
                                                                                                                                                                                                                                                                                                           489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HILL, DAVID E.
KINZLER, KENNETH W.
VOGELSTEIN, BERT
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BURRELL, MARILEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                              202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%; Fr
100.0%; Pr
0;
                                                                                                                                                                                             85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us/08/390,516C
                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                  0,
                                                                                                                                                                                               Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         01107.42798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30;
Pred. No.
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                             DB 1; L
. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; L
3.6e+02;
                                                                                                                                                                                                         Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 489
                                                                                                                                                                                Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
```

```
RESULT 15
US-08-390-515A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
"~+~hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-390-517A-5
                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Applicate Patent No. 5756455
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amin
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KINZLER,
APPLICANT: VOGELSTEI
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                    APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 489 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                   COUNTRY:
                                                                                                                                                    STATE:
                                                                                                                                                                  CITY: WASHINGTON
                                                                                                                                                                                  STREET:
                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 07-APR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 LLLKLLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-508-91
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LLLKLLK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                     20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20001
                                                                                                                                                   D.C
                                                                                                                                                                                                                                                                                                                                                                                      Application US/08390515A
                                                                                                                                                                                  1001 G STREET, N.W.
                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001 G STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOGELSTEIN, BERT
                                                                                                                                                                                                     BANNER, BIRCH, MCKIE AND BECKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BANNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-1993
                                                                                                                                                                                                                                                      HUMAN TUMORS
                                                                                                                                                                                                                                                                    AMPLIFICATION OF HUMAN MDM2 GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%; Score 30;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS
US/08/390,515A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIRCH, MCKIE AND BECKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/390,517A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01107.42798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                 Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; I
. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
```

0,

```
Page 7
```

```
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-390-515A-5
                                                                                                          Db
Search completed: June 17, 2002, 12:42:05 Job time: 225 sec
                                                                                                                                                  δÃ
                                                                                                                                                                                       Query Match 85.7%; Score 30; DB 1; Length 489; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                        2 LLLKLLK 8
|||||||
33 LLLKLLK 39
                                                                                                                                                                                            0;
                                                                                                                                                                                            Gaps
                                                                                                                                                                                            0,
```

THIS PAGE BLANK (USPTO)

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein -
     5
5
7
10
11
                                                                                                                                                                                                                                                                                   and is derived by analysis of
                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length:
                                                                                                                                                                                                 %
Query
Match
                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have ater than or equal to the score of the result being p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
   100.0
100.0
91.4
91.4
91.4
87.1
87.1
78.6
78.6
74.3
74.3
                                                                                                                                                                                                                                                                                                                                                         10:
11:
12:
13:
14:
15:
16:
17:
18:
19:
20:
21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_032802:*
l: /SIDS1/gcgdata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-367-714A-92
70
1 CKLLLKLLLKLLKC '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               June 17, 2002, 12:41:23 ; Search time 94.14 Seconds (without alignments) 16.518 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                | SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
20000000000
     14
77
77
13
13
13
12
12
                                                                                                                                                                                                      ₽B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapext 0.5
                                                                                                                                                                                                                                                                                     of the total score distribution
                                                                                                                                                                                                      ij
AAW82854
AAW82855
AAW82855
AAW82859
AAW82859
AAW35231
AAB17482
AAW35232
AAB17484
AAW35152
AAW35152
                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 4.5
Compugen
             Antipathogenic pep
Antipathogenic pep
Antipathogenic pep
Antipathogenic pep
Diastereomer pepti
Antipathogenic pep
Diastereomer pepti
Antipathogenic pep
Leu/Lys diastereom
Leu/Lys diastereom
                                                                                                                                                                                                   Description
Antipathogenic
                                                                                                                                                                                                                                                                                                   printed
                                                                                                                                                                                                                                                                                                                    b
 pep
```

11111722222222222222222222222222222222	12 13 14
4 1 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	552 522 532
55	74.3 74.3 74.3
12 12 13 13 13 13 13 13 13 13 13 13	12 12 13
211 221 211 211 211 211 211 211 211 211	19 19 21
AABI17483 AABI17485 AAW35150 AAW35150 AAW35169 AAW35170 AAW35171 AAW82848 AAW82885 AAW82885 AAW82886 AAW82886 AAW82886 AAW82886 AAW82886 AAW82886 AAW82886 AAW82886 AAW82887 AABI7414 AABI7417 AABI7420 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI7421 AABI74384 AAW7384 AAW7384 AAW7384 AAW7384	AAW82850 AAW82856 AAB17416
Antipathogenic pep Lytic peptide with Leu/Lys diastereom Antipathogenic pep Membrane active sy KL3 membrane active sy KL3 membrane active sperm whale myoglo Amphipathic peptid Amphipathic peptid Amphipathic peptid Amphipathic peptid Amphipathic peptid Amphipathic peptide with Amino acid sequenc Antimicrobial olig Calmodulin antagon	

ALIGNMENTS

Antipathogenic peptide.

AAW82854;

19-MAY-1999

(first entry)

AAW82854 standard; peptide;

14 À Н

```
AAW82854

ID AAW8

XX X 19-N

XX NON-

XX NON-

XX NON-

XX VOS Synt

XX VOS Synt

XX VOS Synt

XX 27-1

XX 27-1

XX 20-1

XX YOS

XX 
                                                                                                                                                                                                                                                                                                                                                     Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09837090-A1
                                                                                                                                                                                                                                                   1998-594464/50
                                                                                                                                                                                                                                                                                                                                                Ζ,
                                                                                                                                                                                                                                                                                                                                                Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-IL00066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-IL00081
```

New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure

or

Claim 14;

Page

106; 126pp; English.

present peptide is used to produce the agents of the invention.

non-haemolytic,

```
8x 555555555555555555555555555555888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC specification describes a non-haemolytic, cytolytic agent, which is a complex of bundled peptides, a mixture of peptides or a random complex of bundled peptides, a mixture of peptides or a random complex of peptide copolymer. The agent has a selective cytolytic activity on comparison that a selected from a cytolic derivative of a peptide which has a net positive charge greater than 1, comprises I-amino acid residues and comprises an alpha-helix comprises I-amino acid residues and comprises an alpha-helix comprises I-amino acid residues and comprises an alpha-helix comprises I-amino acid residues and I-amino acid residues, has a net consitive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only I-amino acid residues a corresponding amino acid sequence comprising only I-amino acid residues a corresponding bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in the comprision of proposery at the comprision of compresery actives in the constraints productes or compresery actives and compreservatives and compresery actives and compreservatives and compres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                    New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                   Claim 17; Page 106; 126pp; English
                                                                                                                                                                                                                                        WPI; 1998-594464/50.
                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09837090-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antipathogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-haemolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW82858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82858 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cosmetic and food bactericides) or 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                       Shai Y;
peptide is used to produce the agents of the invention. The on describes a non-haemolytic, cytolytic agent, which is a complex of bundled peptides, a mixture of peptides or a random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytolytic; selective cytolytic activity; pathogen;
tion; disinfectant; contact lens wetting solution;
pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                          97WO-IL00066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for preservation of agricultural products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

specification describes a non-haemolytic, peptide, a complex of bundled peptides, a

The present peptide is used to produce the agents of the invention. The specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which

Claim 14;

Page 106; 126pp; English

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                          New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                           WPI; 1998-594464/50.
                                                                                                                                                                                                                                      Oren Z,
                                                                                                                                                                                                                                                                                                                        19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                               Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                             20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a corresponding amino acid sequence comprising only 1-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                    27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                 W09837090-A1
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW82855 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide which has a net positive charge greater than 1, comprises L-amin acid residues and/or D-amino acid residues and comprises an alpha-helix breaker molety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW82855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 cklllklllkllkc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                           97WO-IL00066.
                                                                                                                                                                                                                                                                                                                      98WO-IL00081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70; DB 19;
Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derivative of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

0;

Qy 밁

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-amino acid residues and/or D-amino acid residues and comprises an alpha-helix (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of several diseases caused by pathogens,
                                                                                                                                                                                                                                                                                                                                                                                                        Oren
                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                            continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW82859 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9837090-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-haemolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW82859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cklllklklkllkc 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                           non-haemolytic cytolytic agent useful in treating cancer ections - is a peptide comprising a moiety which disrupts
                                                                                                                                                                                                                                                                                                                                                                      1998-594464/50
                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                            YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molytic; cytolytic; selective cytolytic activity; pathogen; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Shai Y;
                                                                                                                                                                                                                                                        Page 107; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                     peptide is used to produce the agents of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pesticide; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-IL00081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.4%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; I
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

```
SSSSSSK&
     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                including bacterial, fungal, viral, mycoplasma and protozoan. They may be used in both human and veterinary medicine. They used as disinfectants for destruction of microorganisms, i.e. solutions for wetting contact lenses, as preservatives, e.g., cosmetic and food industries, as pesticides (e.g. fungicides of the company of the compan
This sequence represents a diastereomer peptide of the invention. This sequence is used in a "bundle sequence", which is created by binding copies of this sequence to peptide 23 (see AAW35149). The peptides of the invention have: (a) cytolytic activity on pathogenic cells (pathogand malignant cells not naturally present in the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse pathogens. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diastereomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW35231 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                 Peptide(s) having selective and malignant cells, but no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW35231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bactericides) or for preservation of agricultural
                                                                                                                                                                                                                                                                                                                                          WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9731019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                              Example
                                                                                                                                                                                                                                             infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKLLLKLLLKLLKC
|||||| |||||
13 cklllklklkllkc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    տ
                                                                                                                                                                                                                                                                                                                                                                                    Ζ,
                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                           and
                                                                                                                                                                                              Page 49; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pesticide; cell wall lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96IL-0117223
                                                                                                                                                                                                                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [D]-L3,4,8,10-K4L8C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "D-form
                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                 cytolytic activity - haemolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 19
Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 77
                                                                                                                                                                                                                                                                    against pathogens used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungicides or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial cell lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections.
may also be
                                                                        (pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

```
뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides, their complexes and mixtures are used to treat infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as agricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides have few if any toxic effects, and those that include D-aa will have increased resistance to proteolytic degradation. Non-haemolytic, cytotoxic random copolymers of pardaxin, each has a specific spectrum of activity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, resistance
The present invention describes composition of matter (1) comprising Fc domain, pharmacologically active peptides, and linkers. Where (1) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each
                                                                                                                      Claim 39; Page 401; 608pp; English.
                                                                                                                                                    autoimmune diseases
                                                                                                                                                               Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000
                                                                                                                                                                                                                                                                          (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                       23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1 cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antipathogenic peptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       them is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         k111k111k11kc
                                                                                                                                                                                                                                             Ċ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                             Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                            C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                    98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                  99WO-US25044
                                                                                                                                                                                                                                             Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%;
100.0%;
                                                                                                                                                                                                                                          ٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61;
Pred. No.
                                                                                                                                                                                                                                            Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO:586.
                                                                                                                                                                                                                                            TC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
0.013;
                                                                                                                                                              fc domain and
for treating (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                 cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                      an
is:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
```

This sequence sequence is us

used in a "bundle

a diastereomer pundle sequence",

peptide, which i

e of the

invention. This ed by binding 5

created

Example 7; Page 50; 80pp; English.

Peptide(s) having selective and malignant cells, but no

cytolytic activity - against pathogens haemolytic activity, used for treating

and cancer

```
RESULT
AAW35232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                       WPI; 1997-435088/40
                                                                                                                                0ren
                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                 Diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis; agricultural pesticide; cell wall lysis.
                                                                                                                                                                             22-FEB-1996;
                                                                                                                                                                                                     20-FEB-1997;
                                                                                                                                                                                                                                                   W09731019-A2
                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW35232 standard;
                                                                                                                                                                                                                            28-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW35232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             k111k111k11kc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                               Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA;
                                                                                                                                                                              96IL-0117223.
                                                                                                                                                                                                     97WO-IL00066
                                                                                                                                                                                                                                                                                     /note=
10
                                                                                                                                                                                                                                                                                                            /note=
8
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [D]-L3,4,8,10-K5L7C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.1%;
                                                                                                                                                                                                                                                                         "D-form residue"
                                                                                                                                                                                                                                                                                                "D-form residue"
                                                                                                                                                                                                                                                                                                                        "D-form
                                                                                                                                                                                                                                                                                                                                              "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                      residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
```

```
RESULT
AAB17484
   CCCXPSXXT PTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC copies of this sequence to peptide 26 (see AAW35152). The peptides of CC the invention have: (a) cytolytic activity on pathogenic cells (pathogens CC and malignant cells not naturally present in the body); but (b) no CC haemolytic activity, or such activity only at a concentration CC significantly higher than that at which they lyse pathogens. The CC peptides, their complexes and mixtures are used to treat infections CC (caused by bacteria, fungi, protozoa, mycoplasma or viruses) or cancer, CC in human and veterinary medicine. Also, they can be used as preservatives CC for food, cosmetics and agricultural produce, or as agricultural produce, or as agricultural CC pesticides. The absence of haemolytic activity (associated with CC disturbance of alpha-helical structures) means that the peptides have few CC if any toxic effects, and those that include D-ra will have increased CC resistance to proteolytic degradation. Non-haemolytic, cytotoxic random CC copolymers of pardaxin, each has a specific spectrum of activity, CC random copolymers induce total lysis of bacterial cell walls, resistance of habital values to favenian applications. Since these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cance autolimnune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-I; TNF; antac MMP; 'inhibitor; erythropoletin; thrombopoletin; interleukin I cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor
                                                    Claim 39;
                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17484 standard;
The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                  Novel composition of matter comprising an pharmacologically active peptides, useful
                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                       Feige U,
                                                                                                                                                                                                                       (AMGE-) AMGEN
                                                                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                             25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antipathogenic peptide sequence SEQ ID NO:588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor rascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ᆫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       k111k1k1k11kc
                                                                                                                                                                                         Liu
                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unlikely to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                      diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                     Ċ,
                                                   401;
                                                                                                                                                                                                                                                        98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                           99WO-US25044.
                                                                                                                                                                                     Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide; 13
                                                   608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55;
Pred. No.
                                                                                                                                                                                       Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombopoietin; interleukin 1;
igen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                       TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18; Length 13;
0.094;
                                                                                                  Fc domain and
for treating 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

an is

Peptide(s) having selective cytolytic activity - against pathogens

```
RESULT
AAW35149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L4)f-P3-(L3)f-P3-(L4)f-P3-(L3)f-P3-(L4)f-P3-(L3)f-P3-(L3)f-P3-(L4)f-P3-(L3)f-P3-(L3)f-P3-(L4)f-P3-(L3)f-P3-(L3)f-P3-(L3)f-P3-(L3)f-P3-(L3)f-P3-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leu/Lys diastereomer peptide; infection; therapy; excitatory neurotoxin; Honey bee venom; pardaxin; cytoolytic activity; cancer; non-haemolytic; preservative; agricultural produce; bacterial cell lysis agricultural pesticide; cell wall lysis.
                                         WPI; 1997-435088/40
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW35149 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                           (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                     22-FEB-1996;
                                                                                                                                                                                                             20-FEB-1997;
                                                                                                                                                                                                                                                    28-AUG-1997
                                                                                                                                                                                                                                                                                              WO9731019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leu/Lys diastereomer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 klllklklkllkc 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLILKLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                 Shai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                     96IL-0117223.
                                                                                                                                                                                                           97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                 /note=
12
                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%;
92.3%;
                                                                                                                                                                                                                                                                                                                                        "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                          "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                  "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [D]-L3,4,8,10-K4L8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell lysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This sequence represents a Leu/Lys diastereomer peptide of the Ci invention. The peptides of the invention have: (a) cytolytic activity on CC pathogenic cells (pathogens and malignant cells not naturally present in CC the body); but (b) no haemolytic activity, or such activity only at a CC concentration significantly higher than that at which they lyse CC pathogens. The peptides, their complexes and mixtures are used to treat CC infections (caused by bacteria, fungl, protozoa, mycoplasma or viruses) CC or cancer, in human and veterinary medicine. Also, they can be used as CC gricultural pesticides. The absence of haemolytic activity (associated CC with disturbance of alpha-helical structures) means that the peptides CC have few if any toxic effects, and those that include D-aa will have CC increased resistance to proteolytic degradation. Non-haemolytic, CC cytotoxic random copolymers of pardaxin, each has a specific spectrum of CC cutivity, allowing selection of agents for particular applications. Since CC these random copolymers induce total lysis of bacterial cell walls, xxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 12
WO9731019-A2
                                                              Misc-difference
                                                                                     Misc-difference
                                                                                                              Misc-difference
                                                                                                                                                                 Misc-difference
                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW35152;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW35152 standard; peptide;
                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                        agricultural
                                                                                                                                                                                                                                                                                                                   non-haemolytic;
                                                                                                                                                                                                                                                                                                                                  Honey
                                                                                                                                                                                                                                                                                                                                                                      Leu/Lys diastereomer
                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and malignant cells, but no haemolytic activity, used for treating infections and cancer
                                                                                                                                                                                                                                                                                                                                              eu/Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 kllikliiklik 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                           /s diastereomer peptide; infection; therapy; excitatory neurotoxin;
bee venom; pardaxin; cytolytic activity; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Page 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.3%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                      pesticide; cell wall lysis
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĀΑ;
                                                                                   /note=
`11
                                                                                                                                                                                         /note=
                                 /note=
12
                                                                                                                                                                                                                   /note=
                                                             /note=
12
                                                                                                                                                                                                                                                                                                                  preservative; agricultural produce;
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                          /note=
                      /note=
                                                                                                                                                     /note=
                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80pp;
                                                                                                                                                                                                                                                                                                                                                                   peptide [D]-K1,5,9,12L2,6,7,11-K4L8
                       "C-terminal amide'
                                               "D-form
                                                                       "D-form
                                                                                                  "D-form
                                                                                                                          "D-form
                                                                                                                                                   "D-form
                                                                                                                                                                             "D-form
                                                                                                                                                                                                      "D-form
                                                                                                                                                                                                                              "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                              residue'
                                               residue"
                                                                         residue'
                                                                                                  residue"
                                                                                                                          residue"
                                                                                                                                                   residue'
                                                                                                                                                                           residue
                                                                                                                                                                                                     residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 12, 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                bacterial cell lysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spectrum of ations. Since
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

```
AAW82847
Db
                                                                                                                                                                                                                                                                                                                                                                                QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Leu/Lys diastereomer peptide of the invention. The peptides of the invention have: (a) cytolytic activity on the body); but (b) no haemolytic activity, or such activity only at a concentration significantly higher than that at which they lyse concentration significantly higher than that at which they lyse can be peptides, their complexes and mixtures are used to treat infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses) cor cancer, in human and veterinary medicine. Also, they can be used as preservatives for food, cosmetics and agricultural produce, or as capricultural pesticides. The absence of haemolytic activity (associated with disturbance of alpha-helical structures) means that the peptides capricuses of resistance to proteolytic degradation. Non-haemolytic, correased resistance to proteolytic degradation. Non-haemolytic, corresistance to proteolytic degradation as specific spectrum of correct capricultity, allowing selection of agents for particular applications. Since these random copolymers induce total lysis of bacterial cell walls, very constance to them is unlikely to develop.
                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                27-AUG-1998
                                                                                          W09837090-A1
                                                                                                                     Synthetic
                                                                                                                                                          Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution;
                                                                                                                                                                                                     Antipathogenic
                                                                                                                                                                                                                                                                                    AAW82847 standard; peptide;
           20-FEB-1997;
                                      19-FEB-1998;
                                                                                                                                                preservative;
                                                                                                                                                                                                                                  19-MAY-1999
                                                                                                                                                                                                                                                            AAW82847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) having selective cytolytic activity - and malignant cells, but no haemolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-435088/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                       ᆫ
                                                                                                                                                                                                                                                                                                                                                                                 2 KLLLKLLKLLK
                                                                                                                                                                                                                                                                                                                                                       k111k111k11k
                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                           74.3%; S illarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                pesticide;
          97WO-IL00066
                                      98WO-IL00081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96IL-0117223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-IL00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80pp;
                                                                                                                                               fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                contact lens wetting
de; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                        0.
B
                                                                                                                                                                                                                                                                                                                                                                                                                        в 18;
.23;
                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against pathogens used for treating
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Since
```

0;

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The present peptide is used to produce the agents of the invention. The CC specification describes a non-haemolytic, cytolytic agent, which is a CC peptide, a complex of bundled peptides, a mixture of peptides or a random CC peptide copolymer. The agent has a selective cytolytic activity on CC pathogenic cells. The agent is selected from a cyclic derivative of a CC peptide which has a net positive charge greater than 1, comprises L-amino acid residues and comprises an alpha-helix CC comprises 1.-amino acid residues and comprises an alpha-helix CC comprises L-amino acid residues and D-amino acid residues, has a net CC comprises L-amino acid residues and D-amino acid sequence such that a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The crolytric agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, CC cancer or for treatment of several diseases caused by pathogens. They may be used in both human and veterinary medicine. They may also be used in both human and veterinary medicine. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW82850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-haemolytic cytolytic agent useful in treating cancer infections - is a peptide comprising a moiety which disrupts continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used as disinfectants for destruction of microorganisms, i.e. solutions for wetting contact lenses, as preservatives, e.g., cosmetic and food industries, as pesticides (e.g. fungicides c bactericides) or for preservation of agricultural products.
WPI; 1998-594464/50
                               Oren Z,
                                                              (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                            19-FEB-1998;
                                                                                                                                                                                                                                                                      cancer;
                                                                                                                                                                                                                                                                                   Non-haemolytic;
                                                                                                                                                                                                                                                                                                                 Antipathogenic peptide
                                                                                                                                                                                                                                                                                                                                                19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                AAW82850
                                                                                                                                                                                                                                                                                                                                                                                                           AAW82850 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA )
                                                                                             20-FEB-1997;
                                                                                                                                                          27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEDA RES
                                                                                                                                                                                                                                                                    infection;
                                Shai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA,
                                                                                                                                                                                                                                                    pesticide; fungicide; bactericide
                                                                                             97WO-IL00066
                                                                                                                          98WO-IL00081
                                                                                                                                                                                                                                                                                 cytolytic; selective cytolytic activity; pathogen;
                                                                                                                                                                                                                                                                    disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
0.23;
                                                                                                                                                                                                                                                                   lens wetting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                    solution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a corresponding amino acid sequence comprising only L-amino acid residues is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, including bacterial, fungal, viral, mycoplasma and protozoan infections. They may be used in both human and veterinary medicine. They may also be used as disinfectants for destruction of microorganisms, i.e. in solutions for wetting contact lenses, as preservatives, e.g., in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid residues and/or D-amino acid residues and comprises an alpha-helix breaker moiety, or a peptide (or cyclic derivative of this) which (comprises L-amino acid residues and D-amino acid residues, has a net positive charge greater than 1 and has an amino acid sequence such that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification describes a non-haemolytic, cytolytic agent, which is a peptide, a complex of bundled peptides, a mixture of peptides or a random peptide copolymer. The agent has a selective cytolytic activity on pathogenic cells. The agent is selected from a cyclic derivative of a peptide which has a net positive charge greater than 1, comprises L-mino peptide which has a net positive charge greater than 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure
                                                                                                                                                                                                                                                                                               W09837090-A1
                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                             Non-haemolytic; cytolytic; selective cytolytic activity; pathogen; cancer; infection; disinfectant; contact lens wetting solution; preservative; pesticide; fungicide; bactericide.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Antipathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW82856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW82856 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cosmetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
                                                                                                                                                                                                                                                           27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 klliklliklik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present peptide is used to produce the agents of the invention. The product of the invention is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 106; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.3%; Score 52; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
```

New non-haemolytic cytolytic agent useful in treating cancer or infections - is a peptide comprising a moiety which disrupts the continuity of an alpha-helical structure

disrupts the

19-FEB-1998;

(YEDA) YEDA 20-FEB-1997;

RES & DEV CO LTD

97WO-IL00066. 98WO-IL00081.

Ζ,

Shai Y;

Claim 14; Page 106; 126pp; English

peptide is used to produce the agents of the invention.

```
RESULT
AAB17413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc specification describes a non-haemolytic, cytolytic agent, which is a competide, a complex of bundled peptides, a mixture of peptides or a random cc peptide copolymer. The agent has a selective cytolytic activity on cpeptide which has a net positive charge greater than 1, comprises L-amino cc peptide which has a net positive charge greater than 1, comprises L-amino cc peptide which has a net positive charge greater than 1, comprises L-amino cc peptide which has a net positive charge greater than 1, comprises L-amino cc peptide (or cyclic derivative of this) which cc (comprises L-amino acid residues and comprises an alpha-helix cc (comprises L-amino acid residues and latino acid residues, has a net cc positive charge greater than 1 and has an amino acid sequence such that cc is not found in nature. The cytolytic agents may be used for treatment of cancer or for treatment of several diseases caused by pathogens, cc including bacterial, fungal, viral, mycoplasma and protozoan infections. Cc used as disinfectants for destruction of microorganisms, i.e. in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
            autoimmune diseases
               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                        WPI; 2000-350702/30.
                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                           (AMGE-) AMGEN INC
                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                            04-MAY-2000
                                                                                                                                                                                                                                                                                         WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antipathogenic peptide sequence SEQ ID NO:517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17413 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           solutions for wetting contact lenses, as preservatives, e.g., incommetic and food industries, as pesticides (e.g. fungicides or bactericides) or for preservation of agricultural products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                    thrombosis; pharmaceutical
                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                      98US-0105371.
99US-0428082.
                                                                                                                                                                                                                       99WO-US25044.
                                                                                                          Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.3%;
                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB; Pred. No. 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                        Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 12; 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

Claim 39; Page 379; 608pp; English

Novel composition of matter comprising an pharmacologically active peptides, useful

for treat:

and

treating

cancer

WPI; 2000-350702/30

Liu C;

Cheetham

Ĺ

Boone

TC

(AMGE-) AMGEN INC

autoimmune diseases

```
RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \begin{array}{c} \mathbf{x} \\ \mathbf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC (X1)a-F1-(X2)b, where: F1 = an FC domain, plantmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each CC (X1)a-F1-(X2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L4)f-P4 (CC (X1)e-P1-(L2)d-P2-(L4)f-P4), and P4 = are each independently sequences of CC (X1)a-X1 in Axis (X1)a-X1 in 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNP; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antipathogenic peptide sequence SEQ ID NO:520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17416 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 39; Page 378; 608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KLLLKLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21
0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
```

```
CC The present invention describes composition of matter (I) comprising an CC (X1)a-FI-(X2)b, where: FI = an Fc domain; X1 and X2 = aech CC (X1)a-FI-(X2)b, where: FI = an Fc domain; X1 and X2 = aech CC independently selected from -(L1)c-P1 -(L1)c-P1-(L2)d-P2, CC (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P3, or '(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(CC where P1, P2, P3, and P4 = are each independently sequences of CC pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently composition can CC have cytostatic, antiasthmatic, thrombollytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can CC be used for producing pharmaceutical compositions. The compositions are CC useful for treating cancer, asthma, thrombosis, or attoimmune diseases. CC The use of an Fc domain (rather than a Fab domain) can provide a longer that f-ife or incorporate functions such as Fc receptor binding, protein CC Abinding, complement fixation, and possibly placental transfer. AAA69443 CC to AAA6926 and AAB1695 to AAB18003 represent nucleotide and amino acid vy
```

Sequence 12 AA;

Query Match . 74.3%; Score 52; DB 21; Length 12; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

밁 Qγ

Search completed: June 17, 2002, 12:41:23 Job time: 298 sec

THIS PAGE BLANK (USPTO)

```
OM protein -
                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                     ŏ
 Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                               seq
seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                        length:
                                                                                                                                                                                                                                                                                                                                                                                                                length:
                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
       June 17, 2002, 12:43:01; Search time 46.42 Seconds (without alignments) 28.980 Million cell up
                                                                                                                                                                                                                                                                                                                                                               PIR_71:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                        283138 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-367-714A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                               Listing
                                                                                                                                                                                                                                                                                                                                                                                        Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKLLLKLLKLLKC 14
                                                                                                                                                                                                                                                                                                                             pir1:*
pir2:*
pir3:*
pir4:*
                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                2000000000
                                                                481
935
1030
143
230
231
238
375
                                                                                                                                                                                                                                                                                                                                                                              Match 0%
Match 100%
first 45 summaries
                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapext 0.5
                                                                       JC5418
E71375
A60637
H71690
                                                                                                                          AH1734
T41597
                                                                                                                                                                                             G96536
                                                                                                                                                                                                            S50368
                                                                                                          T48285
                                                                                                                                                                   A35650
                                                                                                                                                                                                    T1853
                                                                                                                                                                                   G85043
                                                                                                                                                                                                                                                    Ħ
                                                                                                                   A96914
                                                                                                                                                            A85043
                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.5
Compugen Ltd.
                                                                                                               probable LRR recep
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
uncharacterized pr
                                                                                                                                                                  hypothetical prote
hypothetical prote
intracisternal A p
Sur protein - chic
      small membrane pro
somatolactin - Sen
somatolactin - Jap
prolactin-related
                                     hypothetical prote
hypothetical prote
SEC21 protein - ye
hypothetical prote
                                                                                      somatolactin
probable ABC
                                                                       merozoite antigen hypothetical prote
                                                                                                                                                                                                                                                    Description
                                                                                                          hypothetical
                                                                                                                                                                                                  probable membrane
tractin - medicina
                                                                                                                                                                                                                  hypothetical
hypothetical
                                                                                                                                                                                                                                    nypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell updates/sec
                                                                                                precu
                                                                                                                                                                                                                  prote
prote
prote
                                                                                                         prote
                                                                                         trans
```

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
35	35	ω 5	35	3 5	35	<u>3</u> 5	35	35	<u>3</u> 5	35	36	36	36	36	36
50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	51.4	51.4	51.4	51.4	51.4
394	373	319	318	235	219	179	167	164	125	39	1896	1661	568	438	399
2	N	N	N	Ν	N	N	N	N	N	N	N	N	N	N	N
T19116	T18924	A70102	C81386	A49762	C84647	E75204	H84493	B72717	I50498	G85837	T01490	T31330	T17308	AH0031	T20204
hypothetical	hypothetical	conserved	probable	somatolad	probable	hypothet	probable	hypothetical	urotensin II	hypothetical	hypothetical	head-acti	hypotheti	proton gl	hypotheti
	ical prote	conserved hypothet	probable integral	somatolactin precu	probable synaptobr	ypothetical prote	robable replicati	ical prote	n II-alpha	ical prote	ical prote	ead-activator bin	pothetical prote	roton glutamate s	ical prote

ALIGNMENTS

```
A; Molecule type: DNA
A; Residues: 1-169 < ARN>
A; Residues: 1-169 < ARN>
A; Residues: 1-169 < ARN-
A; Cross-references: GB: AE001613; GB: AE001363; NID: 94376550; PIDN: AAD18426.1; PID: 9437
A; Experimental source: strain CWLO29
A; C:; Dodson, R:; Gwinn, M:; Nelson, W:; DeBoy, R.; Kolonay, J:; McClarty, G:; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                              R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: G72096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein CP0481 [imported] - Chlamydophila pneumoniae (strains CWL029 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: Appr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: G72096; C81573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Z1386 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: B85632 C;Accession: B85632 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mailler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B85632
A; Reference number: A; Accession: C81573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: Z13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-38 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B85632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEILVNILLKMIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 42.9
6; Conservative
                            A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE005174; NID:g12514232; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB Pred. No. 2.1; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAG55518.1; GSPDB:GN00145; UWGP:n EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

```
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Status: nralimits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <REA>
A;Cross-references: GB:AE002209; GB:AE002161; NID:g7189393; PIDN:AAF38311.1; PID:g718939
A;Cross-references: Strain AR39, HL cells
                                                                A; Map position: .12R
C; Keywords: transmembrane protei
F; 263-279/Domain: transmembrane
                                                                                                                                                                                                                                                           N;Alternate names: hypothetical protein L8003.9
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: S50368
R;Pauley, A.
submitted to the EMBL Data Library, November 1994
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-314 <PAU>
A; Cross-references: EMBL:U17243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CPj0277
C;Superfamily: Chlamydia pneumoniae hypothetical
                                                                                                                      A; Gene: MIPS:YLR283w
                                                                                                                                      A;Cross-references:
C;Genetics:
                                                                                                                                                                                                         A; Reference number: S50366
A; Accession: S50368
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:BA000008; NID:g8978651; PIDN:BAA98487.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-169 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Chlamydophila pneumoniae, Ct
C;Date: 02-Mar-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CPn0277; CP0481
C;Superfamily: Chlamydia pneumoniae hypothetical
                                                                                                                                                                                                                                           A; Description: The sequence
                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YLR283w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein CPj0277 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E86525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 
nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LLIKLLKLIKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPj0277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
                                                                                                                                                                                                                                        to the EMBL Data Library, November ion: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|::::||:||
LVLQVIIKLIKC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVLQVIIKLIKC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLIKLLKLIKC 14
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 50. 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
57.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%;
50.0%;
                                                                                    protein
                                                                #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
6; Mis
                                                                                                                                                       NID:g596030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                  predicted
40;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
23;
ДВ
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
23;
                                                                                                                                                                                                                                                          1994
                                                                                                                                                                                                                                        cosmid 8003
                                                                                                                                                     PID:g596039; GSPDB:GN00012; MIPS:YLR283w
            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein CPn0277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein CPn0277
                                                                  <MMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
              Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.;
```

RESULT 7
G85043
hypothetical
C; Species: A

nl protein AT4g03450 Arabidopsis thaliana

[imported]

Arabidopsis thaliana

```
C; Accession: G96536
C; Accession: G96536
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, F.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Hirudo medicinalis (medicinal leech)
C;Decies: Hirudo medicinalis (medicinal leech)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C;Accession: T18531
R;Huang, Y; Jellies, J; Johansen, K.M.; Johansen, J.
J. Cell Biol. 138, 143-157, 1997
A;Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-sta;Tatle: Difference number: Z18951; MUID:97362067
A;Accession: T18531
A;Accession: T18531
    밁
                                    Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F2J10.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
T18531
                                                                                                                                                                       A; Map position:
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-2513 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1880 <HI
A; Cross-references: El
                                                                                                                                                                                            A; Gene: F2J10.9
                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                  A;Cross-references:
                                                                                                                                                                                                                                                                                           A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tractin
                                                                                               Query Match
Best Local Similarity
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1758
797 LLLGLLLKLLK 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 9; Conserv
                                      3 LLLKLLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - medicinal leech
es: Hirudo medicinalis (medicinal leech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                         preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTTTTTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKITTALLLQLL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKLLLKLLKLL 12
                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <HUA>
                                                                                                                                                                                                                                  GB:AE005173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: U92813; NID: g2275259; PID: g2275260; PIDN: AAC47654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                               57.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
64.3%;
                                                                                                                                                                                                                                NID: g8569097; PIDN: AAF76442.1;
                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                               Score 40;
Pred. No.
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
1.7e+02;
                                                                                                                   DВ
                                                                                               .1e+02;
                                                                                                                 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۳
                                                                                                               Length 2513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1880;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                  GSPDB: GN00141
                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel Ig-superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              R.;
                                                                                                                                                                                                                                                                                                                                                                                        Η.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.;
                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dewar,
                                                                                                                                                                                                                                                                                                                                                                                          Tallo
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alon
```

```
C;Genetics:
A;Gene: AT4g03450
A;Map position: 4
                                                                                                           Sur protein - chicken
C;Species: Gallus gallus (chicken)
C;Becies: Gallus gallus (chicken)
C;Bate: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C;Bate: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C;Baccession: A35650
R;Dorai, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
Mol. Cell. Biol. 10, 4068-4079, 1990
                                                                               A;Title: An alternative non-tyrosine protein A;Reference number: A35650; MUID:90318371 A;Accession: A35650
                                                                                                                                                                                                                                                                     RESULT
A35650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intracisternal A particle GAG protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: B44314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Sequence and analysis of chromos
A; Reference number: A85001; MUID:20083488
A; Accession: G85043
                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence: C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A44314; MUID:93054523
A;Accession: B44314
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Brigle, K.E.; Westin, E.H.; Houghton, M.T.; Goldman, I.D.
J. Biol. Chem. 267, 23351-22355, 1992
A;Title: Insertion of an intracisternal A particle within the 5'-regulatory region of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-641 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: G85043
R;anonymous, The European Union Arabidopsis Genome
Nature 402, 769-777, 1999
                     A; Molecule type: mRNA
A; Residues: 1-219 < DOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: L1210 leukemia cells LL1 subline A; Note: sequence inconsistent with the nucleotide trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA;
A; Residues: 1-30 <BRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
    A; Cross-references:
                                                         A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ith increased protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304
                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:117028, ; family: AIDS-related virus gag polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
sion: G85043
                                                                                                                                                                                                                                                                                                                                                                                           1 CKLLLKLLKLL
                                                                                                                                                                                                                                                                                           φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKIFLKLLKC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                     CYLVLKLGLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
GB:M57290; NID:g212703; PIDN:AAA49076.1; PID:g212704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:NC_001268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB
Pred. No. 1e+(
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID:g7270215; PIDN:CAB77830.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBIP:117029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-Apr-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Cold
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                        'n
                                                                                                                        chicker
```

Query

Match

54.3%;

Score

38;

DB

2

Length 219;

```
hypothetical protein F08B12.3a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #texi C;Accession: T20577
                                                                RESULT
T20577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F08B12.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable LRR receptor-like protein kinase [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: A85043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
A85043
                                                                                                                           밁
                                                                                                                                                     Qy
                                                                                                                                                                                                                                                              A; Map position: X
A; Introns: 38/2; 64/1; 112/2; 148/3; 173/3; 201/3; 348/3;
                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data A; Reference number: Z19295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; anonymous, \ \mbox{The European Union Arabidopsis Genome Sequencing Consortium, The Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-1107 <WIL>
A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T20578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T20578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-754 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A85001; A; Accession: A85043
                                                                                                                                                                                                                                                                                              A; Gene: CESP:F08B12.3b
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Dobson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T20578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: AT4g03390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Sequence and analysis of chromosome 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                  Query Match
                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 CELMIKCGLVLLQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                     Local
                                                                              12
                                                                                                                                                       1 CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLLLKLLKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              سا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 CLLLLPLLLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKLLLKLLKLLKC
                                                                                                                           CNVLIKLLTCILYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary
                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 50.07; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
9; Conserv
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                              EMBL: Z68104;
ce: clone F081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:NC_001268; NID:g7270209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                           83
                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.3%;
75.0%;
                                                                                                                                                                                                    54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUID: 20083488
                                                                                                                                                                                                                                                                                                                                            PIDN:CAA92116.1; GSPDB:GN00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB
Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                                                                                        November
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                     DB 2;
2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:CAB77824.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų.
                                                                                                                                                                                                                    Length 1107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                  392/2; 452/1; 488/2; 538/2;
                   18-Feb-2000
                                                                                                                                                                                                                                                                                                                                              CESP: F08B12.3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPDB: GN00140
                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cold
```

```
A;Cross-references: EMBL:AL031825; PIDN:CAA21231.1; GSPDB:GN00068; SPDB:SPCC757.06 A;Experimental source: strain 972h-; cosmid c757 C;Genetics:
                                                                 A; Molecule type: DNA
A; Residues: 1-116 <LYN>
                                                                                                    A; Status: preliminary; translated
                                                                                                                                                     R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, submitted to the EMBL Data Library, October 1998
A;Reference number: Z22003
                                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
"hehes 7; Conservations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein lin2421 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (C;Species: Listeria innocua (C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1734 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
                                                                                                                                  A; Accession: T41597
                                                                                                                                                                                                                                                                          hypothetical protein SPCC757.06 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1119 <WIL>
A; Cross-references: EMBL: 268104; PIDN: CAA92115.1; GSPDB: GN00028; CESP: F08B12.3a
A; Experimental source: clone F08B12
C; GenetLcs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: lin2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL592022; PIDN:CAC97648.1; PID:g16414943; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-83 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: X
A;Introns: 38/2; 64/1; 112/2; 148/3; 173/3; 201/3; 348/3; 392/2; 452/1; 488/2; 538/2; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z19295
A;Accession: T20577
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Dobson, R. submitted to the EMBL Data Library, November 1995 A:Reference number: Z19295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:F08B12.3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                 4 LLKLLLKLLKC 14
:| || |:|||
50 MLPLLAKILKC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 50.0 hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CKLLLKLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNVLIKLLTCILYC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω,
                                                                                                      from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maitournam, A.; Ma
Voss, H.; Wehland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Bloecker
Fsihi, H.
```

Search completed: June 17, 2002, Job time: 257 sec

12:43:02

д

40

RFLLKLLRKLIK

```
Ş
                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <KUR>
                                                                                                                            RESULT
A96914
                                                                A; Gene:
                                                                               A;Cross-references: GB:AE001437; PIDN:AAK78100.1; A;Experimental source: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                              A;Gene: SPDB:SPCC757.06
A;Map position: 3
A;Introns: 10/3; 48/3
                  Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.4
Conservative
                                                                         Genetics:
                           Local Similarity
                                                                                                                                                                                                                                                               82
2 KLLLKLLKLLK 13
                                                                CAC0115
                                                                                                                                                                                                                                                                               2 KLLLKLLKLLKC 14
                                                                                                                                                                                                                                                              KFLIKLIVKMTDC
                  Conservative
                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                         52.9%;
                           52.9%;
                 ?
                         Score 37; DB
Pred. No. 58;
                                                                                                                                                                                                                                                                                                         Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                 core 37; DB red. No. 51; Mismatches
                 Mismatches
                                  2;
                                                                                                                                                                                                                                                                                                                  2;
                                                                               PID:g15022941; GSPDB:GN00168
ATCC824
                 ?
                                  Length 137;
                                                                                                                                                                                                                                                                                                                  Length 116;
                Indels
                                                                                                                                                                                                                                                                                                Indels
               0;
                                                                                                                                                                                                                                                                                                0,
               Gaps
                                                                                                                                                                                                                                                                                              Gaps
              0;
                                                                                                                                                                                                                                                                                               0;
```

THIS PAGE BLANK (USPTO)

í

drosophila bacillus su mus musculu rattus norv

streptococc

buchnera ap

```
OM protein - protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-367-714A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKLLLKLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
20000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 0%
Match 100%
first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002, 12:44:47; Search time 21.35 Seconds (without alignments) 25.390 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapext 0.5
                                                                                               PRRA_RAT
RPSE_CLOAB
SHBG_RAT
                                                                                                                                                                                 SOML_TETMU
SOML_SPAAU
SOML_SCIOC
SOML_SCIOC
SOML_CARAU
LOFAL FIMTE
COPE_YEAST
EAG_BACSU
Y035_TREPA
Y035_TREPA
Y035_TREPA
Y035_TREPA
Y035_TREPA
Y035_TREPA
Y035_TREPA
Y035_TREPA
SOML_HIPHI
SOML_SOUSE
SOML_HOHI
Y147_MYCGE
SOML_PAROLI
Y147_MYCGE
CCAH_HUMAN
UR2A_CYPCA
SOML_GADMO
MTGA_KLEPM
UR2A_CYPCA
SYYM_YEAST
YDK9_SCHPO
OTOF_HUMAN
RIFL_YEAST
UR2G_CYPCA
IGF_MYXGL
IGF_MYXGL
IGF_MYXGL
ECPJ_MOUSE
                                      XTMB_BACSU
CDS1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P54863 sparus aura
P79894 sparus aura
O9ygk7 sciaenops o
O9pwg4 siganus gut
P79697 carassius a
O83078 treponema p
P15714 eimeria ten
      P20362
P47393
P054180
P05180
P095180
P093262
P21919
P48465
P48527
P48527
P48527
P48527
P095115
P095115
P095116
P095116
P09517
P0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q919h4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P45642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P45641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P06630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                O cyprinus ca
2 acipenser t
9 gadus morhu
5 klebsiella
7 saccharomyc
g saccharomyc
cyprinus ca
myxine glut
mus musculu
rattus norv
clostridium
rattus norv
bacillus su
schizosacch
gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 solea seneg
paralichthy
bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mycoplasma
homo sapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hippoglossu
solea seneg
                                                                                                                                                                                                                                                                                                          schizosacch
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             saccharomyc
bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tetraodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapien
                                                                                                                                                                                                                                                                                                    RESULT 1
SOML_TENU
ID SOML_TENU
ID SOMLT
AC Q919H4
AC Q919H4
DT 01-MAR
DT 01
                                      В
                                                                                        Qy
                                                                                                                                                  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                       CHAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CERBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444
444
444
444
444
444
444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and sequencing of Tetraodon miurus somatolactin."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: PITUITARY GLAND.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon miurus (Congo puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
NCBI_TaxID-94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone; 1. PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Creat
01-MAR-2002 (Rel. 41, Last
01-MAR-2002 (Rel. 41, Last
Somatolactin precursor (SL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00266; SOMATOTROPIN_1; PROSITE; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF253066; AAF64522.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pituitary;
Rand-Weaver M., May D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q919H4;
                                      211
                                                                                            5 LKLLLKLLKC 14
                                  IEILLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _TETMU
                                                                                                                                                                                                                                                                 3; Glycoprotein; S
1 21
22 229
3 26 36
87 203
220 228
143 143
229 AA; 26125 M
                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.6
48.6
48.6
48.6
48.6
48.6
48.6
47.1
147.1
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515
576
742
821
821
901
984
986
1333
31
31
93
                                                                                                                                                                                 57.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal
                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                       POTENTIAL.
SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLTA_STRMU
ACH2_DROME
PURL_BACSU
TRKB_MOUSE
TRKB_RAT
                                                                                                                                                     Score 40; DB Pred. No. 12; 3; Mismatches
                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPL_BUCRP
YO08_BPHP1
PD11_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHSG_YEAST
DPOL_NPVAC
DPOL_NPVBM
CC25_CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                        0;
                                                                                                                                                                                                              Length 229,
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q53526
P17644
P12042
P152042
P15209
Q63604
P06738
P18131
P41712
P43061
P41712
P43061
P553017
P51709
                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          saccharomyc
lautographa
bombyx mori
candida alb
```

Result

Ö

Score

Query Match

Minimum

DB DB

seq

length: length:

Minimum Match

Maximum

Total number of

105224 seqs,

Database

score and is

is

Title: Perfect score:

on:

June

17,

Scoring table: Sequence:

BLOSUM62

10.0,

Gaps

0,

 $\begin{smallmatrix} 555 \\ 557 \\ 55$

us-09-367-714a-92.rsp

```
Query Match 57.1
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
"SOM2_SPAAU STANDARD; PRT; 231 AA.
P78934;
01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
01.MAR-2002 (Rel. 41, Last annotation update)
Somatchactic 2 prequisor (SL),
Sparus aurata (Gilthead sea bream)
Actinopterygii; Neoplesygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE Pituitary
MEDLINE-9714443, PubMed-8954766;
Astola A., Pendon C., Ortiz M., Valdivia M.M.;
Cidening and expression of sometolactin a pituitary hormone related to growth hormone and prolactin from glithead seabream, Sparus aurata, Comp. Endocrinol. 104:330-336(1996).

10 SUBCELLUAR LOOPINON: SECRETED TO THE SOMATOTROPIN/PROLACTIN FAMILY.

11 TISSUE SPECIFICITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oi-Oci-1996 (Rel. 34, Created)
Oi-Oci-1996 (Rel. 34, Liast sequence update)
15-JUL-1999 (Rel. 38, Liast annotation update)
Somatolactin i precursor (SL).
Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii, "Peleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Sparus.
NCBI_TaxID-8175;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L49205; AAA98734.1; -. HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOM1_SPAAU
P54863;
                                                                                                                                                                                                                                                                                                                                                               213 MEILLKLLKC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            5 LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "S; PR00836; SOMATOTROPIN.
"E; P800266; SOMATOTROPIN.1; 1.
"E; P$00236; SOMATOTROPIN.2; 1.

1E; P$00338; SOMATOTROPIN.2; 1.

1E; Glycoprotein; Signal POTENTIAL.
25 231 SOMATOLACT1
D 29 39 BY SIMILARI
D 29 205 BY SIMILARI
D 29 20 BY SIMILARI
D 29 23 BY SIMILARI
D 29 25 BY SIMILARI
D 29 25 BY SIMILARI
D 29 25 BY SIMILARI
D 29 27 28 BY SIMILARI
D 29 28 BY SIMILARI
D 31 145 N-T-TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 231; Pred. No. 12; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POPTENTIAL.
SOMATOLACTIN 1
SOMATOLACTIN 1
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
N-LINKED (GLCNAC. . .) (POTENTIAL).
1; 67A4457D43E02504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
RESULT 4
SOMIL_SCOOL
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 09YGKZ
AC 01-MAA
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŷ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.:
Best Local Similarity 70.0
Matches 7; Conservative
                                     Somatolactin precursor (SL).
Schaenops ocellatus (Red drum).
Schaenops ocellatus (Red drum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Peleostei; Euteleostoi; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Schaenidae; Schaenops.
NCPI_TaxID-76340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y11144; CAA72031.1; -. HSSP; P01246; IBST.
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acanthomorpha; Ac
Sparidae; Sparus.
NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 MEILLKLLKC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSCIOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 231; Pred. No. 12; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
```

231 AA

0; Gaps

0

RESULT
SOM2_SP
ID M2_SP
ID P
AC P
DT 0
DT 0
DT 0
DT 0
OC S
OC F
OC F

B Ş

```
PROBLEM 18 OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
SOMATOLACTIN 2
SOMATOLACTIN 2
BY SIMILARITY
BY SIMILARITY
N-LINKED (GLCNAC . ) (POTENTIAL).
1, 09C774C6BDE0BBA1 CRC64;
```

_

```
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PWG4;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
          PROSITE;
                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Acanthuroidei; Siganidae; Siganus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                   EMBL; AB026186; BAA83467.1; Interpro; IPRO01400; SOMATOTROPIN. Pfam; PF00103; hormone; 1. Pfam; PF00103; hormone; 1. PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                 "Isolation and cDNA cloning of somatolactin guttatus).";
                                                                                                                                                                                                                                                                                                            Ayson F.G., de Jesus
Kawauchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somatolactin precursor (SL).
Siganus guttatus (Rabbitfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                       -1: SUBCELLULAR LOCATION: Secreted.
-1: TISSUE SPECIFICITY: PITUITARY GLAND.
-1: SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                       Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                                         TISSUE-Pituitary;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOML_SIGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF062520; AAD17534.1;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=92439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEILLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conser
        PS00266; SOMATOTROPIN_1;
PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00266; SOMATOTROPIN_1; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
89
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                   1999) to the EMBL/GenBank/DDBJ
LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.18;
70.08;
                                                                                                                                                                                                                                                                                                                          E.T., Amemiya Y., Moriyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
4FB039DEE6EDBD01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on 
ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۳.
                                                                                                                                                                                                                                                                                                in rabbitfish (Siganus
                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and the
                                                                                                                                                                                                                                                                                                                           S., Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

DЬ Ş

210

IQTLLKLLKC 219 LKLLLKLLKC

Ŋ

14

```
RESULT 6
SOML_CAAD
ID MSCOML_O
AC P79697
DT 01-NOV
DT 01-NOV
DT 15-UII
DE CARASS
OC CAPTIC
OC CAPTIC
OX CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                          Hormone;
SIGNAL
CHAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-97242175; PubMed=9125164;

Cheng K.W., Chan Y.H., Chen Y.D., Y

"Sequence of a cDNA clone encoding

Carassius auratus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P79697;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                           Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                                                                             EMBL; U72940;
HSSP; P01246;
                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Somatolactin precursor
                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 232:282-287(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOML_CARAU
                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEILLKLLKC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKLLLKLLKC 14
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conser
                                                                                                                                                                                                                     Glycoprotein; Signal
                                                                                                                                                                                                                                     PS00266; SOMATOTROPIN_1; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                            IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 (Rel. 35, Create
7 (Rel. 35, Last of
9 (Rel. 38, Last of
                                                                                     24
28
87
219
219
226
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
25
29
89
222
222
145
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                AAC60098.1;
                                                                                         A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                          230
38
202
227
226
25735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
231
205
205
230
145
                 52.9%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                         W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence up
                                                                                     SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POT NO. CBC5DB347C6116DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
••
۶,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB
Pred. No. 12;
3; Mismatches
                 Score
Pred.
                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09A9CD5EE13840AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu
                                                                                                                                                                                                                                                          FALSE_NEG
               37;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update]
               36;
                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                          as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chan K.M.;
somatolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
1;
                                  Length 230,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                         рy
                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration .
MBL outstation .
 0;
                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                         ons on its in no way commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
 0,
```

```
AC DT DT DT DT OC
                                                                                                                                                                         RESULT
LP61_E
                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y035_T
                                                                          01-APR-1990
01-APR-1990
01-FEB-1994
                  Eukaryota;
                                    Antigen LPMC-61
Eimeria tenella
                                                                                                                                   LP61_EIMTE
P15714;
                                                                                                                                                                         EIMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
NP_BIND 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001188; AAC65030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y035_TREPA
083078;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spirochete.";
Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM
TP0035/TP0035/TP0036 FOR A METAL. PROBABLY RESPONSIBLE FOR ENERGY
COUPLING TO THE TRANSPORT SYSTEM.
SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                             LLKLLKLLK 13
                                                                                                                                                                                                                                              LVKLVLKLLK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00005; ABC_tran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP0035;
                                                                                                                                                                                                                                                                                                                         Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00211; ABC_TRANSPORTER; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003439; ABC_transportr.
IPR001687; ATP_GTP_A.
Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                      (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                    (Fragment).
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       el. 40, Last annotation update)
transport system ATP-binding protein TP0035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                14, Created)
14, Last sequence up
28, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                              51
26460 MW;
                                                                                                                                                                                                                                                                                                                                   52.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                   Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                        673E7B4882BE4D29 CRC64;
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inner membrane; ATP-binding;
                                                                                         update)
                                                                                                                                             255 AA.
                                                                update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                     DB
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                 Length 238;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOLUTION OF THE TRANSPORMENT OF THE TRANSPORME
                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                         B
```

```
RESULT OF COPG_YEAST ID COPG_Y AC P32074 DT 01-OCT DT 16-OCT DE Coatom GN SEC21 OS Saccha OC Eukary OC Saccha OX NCBL_T RN [1]
RP SEQUEN
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                              P32074;
01-OCT-1993 (Rel. 2
01-OCT-1996 (Rel. 3
16-OCT-2001 (Rel. 3
                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                 Coatomer gamma subunit (Gamma-coat SEC21 OR YNL287W OR N0543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
NON_TER
                                                                                                                                                                                                          COPG_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M30933; AAA29079.1; PIR; A60637; A60637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of a target antigen of a monoclonal antibody directed against Eimeria tenella merozoites."; MOI. Biochem. Parasitol. 41:53-64 (1990)
-!- FUNCTION: UNKNOWN. THE GLN-RICH TANDEM REPEATS MAY BE IMPORTANT FOR AN UNKNOWN ASPECT OF THE PARASITIC LIFE CYCLE. MAY BE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90348718; PubMed=2200963; Ko C., Smith C.K. II, McDonell M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Sporozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             2 KLLLKLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MAY BE COVALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO FORM THE 80 kDa ANTIGEN.
DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE SPORULATION OF THE OCCYSTS AND IN THE SPOROZOITES FOLLOWING
                                                                                                                                                                                                                                                                                            RLLLKLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXCYSTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT IMMUNOGEN
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sporozoite;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                          12
                                                                                                   27, Created)
34, Last sequence update)
40, Last annotation update)
...** 'Gamma-coat protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                           210 1:
255
31267 ·MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103
140
152
164
172
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
57
65
78
90
                                                                                                                                                                                                                                                                                                                                                                           52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                                                                         Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 X
                                                                                                                                                                                                                                                                                                                                                                                                                                          8C5E6005FFFC2DB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPROXIMATE
                                                                                                                                                                                                                                                                                                                                                                         DВ
39;
                                                                                                                                                                                                  Ą
                                                                                                              (Gamma-COP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                                                                      Length 255;
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                 0;
```

SEQUENCE FROM N.A NCBI_TaxID=4932;

```
В
                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                    _BACSU
                                                                                                                                                                                         P06630;
01-JAN-1988
01-JAN-1988
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Protein transport; Golgi stack; Membrane.
CONFLICT 353 353 D -> N (IN REF. 1).
SEQUENCE 935 AA; 104830 MW; 99DC7D737D4EF761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002553; Adaptin_N.
Pfam; PF01602; Adaptin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M59708; AAA34598.1; -.
EMBL; Z71563; CAA96204.1; -.
PIR; A33151; A33151.
PIR; S28915; S28915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosobuchi M.M., Kreis T., Schekman "SEC21 is a gene required for ER to encodes a subunit of a yeast coator
MEDLINE-88260878; PubMed-2838724; Perego M., Hoch J.A.; Pschlation and sequence of the sp sporulation in Bacillus subtilis.
                                                                                                                Bacillus subtilis.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1996) to the -i- FUNCTION: THE COATOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glansdorff N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                            STRAIN-168;
                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                    EAG_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Messenguy F., Dubois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 360:603-605(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93096049; PubMed=1461285;
                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                      1 CKLLLKLLKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUNCTION: THE CÓATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSVINHETIC
PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLG
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
VESTCLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE COPG FAMILY.
                                                                                                                                                                                                                                                                                                                          CRLLISRLLRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S0005231; SEC21.
                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conser
                                                                                                                                                                             (Rel.
(Rel.
(Rel.
(Rel.
1 16.4
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                    STANDARD; .
                                                                                                                                                                             06,
40,
40,
                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                               52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E., Vierendeels F.,
                                                                                                                                                                        Last sequence update)
Last annotation update)
protein in SPOOE 3'region.
                                                                                                                                                                                                                       Created)
                                                                                                                  Bacillus/Clostridium group; s group; Bacillus.
 of the spoOE gene: subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB
Pred. No. 1.3e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c ER to Golgi protein transport that
coatomer.";
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.;
                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                              1.3e+02;
2;
                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scherens
               its
                                                                                                                                                                                                                                                                                                                                                                                                            Length 935;
               role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В.,
               in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pierard
               initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d for
                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOLGI
                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
RESULT 11
SOML_HIPHI
    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          Hormone;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatolactin precursor (SL).

Hippoglossus hippoglossus (Atlantic halibut).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Hippoglossus.

NCBI_TaxID-8267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Sporulation; Complete proteome. SEQUENCE 143 AA; 16429 MW; D7410B50963D7A75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00526; CAA68584.1;
EMBL; Z99111; CAB13238.1;
PIR; S03747; S03747.
SubtiList; BG10770; eag.
                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement into tremoved. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      "Iraqi F., Gong Z., Hew C.L., Crim L.W.;
"Isolation and characterization of somatolactin genes
water marine teleosts, lumpfish (Cyclopterus lumpus) a
(Hippoglossus hippoglossus).";
(Hippoglossus hippoglossus).";
                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=93372995; PubMed=7689905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P45641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOML_HIPHI
                                                                                                                                                         EMBL; L02117;
HSSP; P01246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 1:125-132(1987).
                                                                                     PROSITE;
                                                                                                    PROSITE;
                                                                                                                 PRINTS; PR00836;
                                                                                                                                                                                                                                                                        between
                                                                                                                                            [nterPro; IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 LLLKMLLRFIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LLLKLLLKLLK
                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                              . Mar. Biol. Biotechnol. 2:96-103(1993).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                PF00103;
                                                                        Glycoprotein;
                                                                                  PS00266; SOMATOTROPIN_1; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
 24
28
88
221
                                                                                                                                                                        AAC38003.1;
                                                                                                                                                            1BST
                                                                                                                hormone; 1.
6; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
 23
230
38
204
229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.4%;
                                                                        Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
--
POTENTIAL.
SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 AA
                                                                                                                                                                                                                                            There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                         from two cold
and halibut
                                                                                                                                                                                                                                                                         EMBL
                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

DISULFID DISULFID DISULFID

```
RESULT
SOML_SO:
g
                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS
                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                              Query Match
Best Local
                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                            DISULFID DISULFID DISULFID CARBOHYD CARBOHYD SEQUENCE
                                                                                                                                                                                                                                                                                                                     Hormone;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 senegalensis).";
Gene 147:227-230(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solea senegalensis (Sole).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Soleoidei; Soleidae; Solea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95011619; PubMed-7926805;
Pendon C., Martinez-Barbera J.P., Valdivia M.M.;
"Cloning of a somatolactin-encoding cDNA from so senegalensis).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Somatolactin precursor (SL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P45642;
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U06753; AAA61873.1;
HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOML_SOLSE
                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=28829;
                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro; IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LKLLLKLLKC
                                     ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: PITUITARY GLAND.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                     LKLLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEIFLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                      PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                        PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
6; Conser
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                        Glycoprotein;
1 23
                                                                                                                                                                                                                                                                                                                                                                PS00338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
144
230
                                                                                                                                                                                                                    24
28
88
221
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                     14
                                                                                                                                                                                                                                                                                                                                                           SOMATOTROPIN_1;
SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
144
26519
                                                                                                                                                                            144
26586
                                                                                                                                                                                                                    204
229
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%;
                                                                                                   51
60
                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                 .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W.
                                                                                                                                                                               WW;
                                                                                                                                                                        POTENTIAL.

SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

BY SIMILARITY.

OF COLUMN (POTENTIAL COLUMN (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB Pred. No. 51; 3; Mismatches
                                                                              ω
--
                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
; 1E3C16622F75946A CRC64;
                                                                              Mismatches
                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sole (Solea
                                                                              1;
                                                                                                                 Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230,
                                                                                                                                                                                                  .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þу
                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

```
RESULT 13
SOML_PAROL STANDARD
ID SOML_PAROL STANDARD
AC P20362;
DT 01-FEB-1991 (Rel. 17, C
DT 01-FEB-1991 (Rel. 17, L
DT 01-NOV-1995 (Rel. 32, L
                                                                                                                                                                                                                      DACTO
                                                                                                                   밁
                                                                                                                                       ş
                                                                      RESULT 14
PRR1_BOVIN
                                                                                                                                                              Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Somatolactin precursor (SL).

Paralichthys olivaceus (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M33696; AAA49445.1; -.
EMBL; M33695; AAA49444.1; -.
PIR; A35793; A35793.
HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
              01-NOV-1988
01-NOV-1997
                                      01-NOV-1988
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S-1- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawauchi H.;
"cDNA cloning of somatolactin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ono M., Takayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pituitary;
                                               P05402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hormone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90272707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8255;
                                                            PRR1_BOVIN
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00836; SOMATOTROPIN
                                                                                                                                                                                                                                                                                                      Hormone;
                                                                                                                   213
                                                                                                                                       5 LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: PITUITARY GLAND. SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                   MEIFLKLLKC
                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                               PS00266;
PS00338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.,
                                                                                                                                                                                                                                                                                                      Glycoprotein;
(Rel. 09, Created)
(Rel. 09, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin.";
                                                                                                                                                                                                                                              25
29
89
222
                                                                                                                                                               Conservative
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                               SOMATOTROPIN_1;
SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2349240;
                                                                                                                                                                                                                                  24
231
39
205
230
145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                        26731
                                                                                                                                                                          51.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rand-Weaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                      SOMATOLACTIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                               ω
                                                                                                                                                               Score 36; DB Pred. No. 52; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87:4330-4334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Χ
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pituitary protein related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      얽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
                                                             238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
                                                                                                                                                                                      ب
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                      Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasunaga T.,
                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ЬY
                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     for commercial
                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noso T.,
                                                                                                                                                                Gaps
                                                                                                                                                                0;
```

prolactin-related

```
RESULT
Y147_MY
ID Y1
AC P4
DT 01
DT 16
DT 16
GN MC
                                                                                                                                                 В
                                                                                                                                                                     Š
                                                                                                                                                                                                                                                          Best Local
Matches
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J02944; AAA30726.1; EMBL; M25494; AAA30727.1; J
EMBL; M25491; AAA30727.1; J
EMBL; M25492; AAA30727.1; J
EMBL; M25492; AAA30727.1; J
EMBL; M25493; AAA30727.1; J
PIR; A31417; A31417.
                                   01-FEB-1996
01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                       DISULFID
DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-89251077; PubMed-2721368;
MEDILINE-89251077; PubMed-2721368;
Ebbitt D.M., Hurley W.L., Kessler M.A., McDonald D.J., Schuler L.A.;
"Characterization of the gene corresponding to bovine placental prolactin related cDNA I: evolutionary implications.";
DNA 8:161-169(1989).
-I- FUNCTION: PLACENTAL PROLACTIN-RELATED PROTEINS MAY PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Hypothetical MG147.
                                                                        Y147_MYCGE
P47393;
                                                                                                 MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=87289662; PubMed=3475696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                               formone;
                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schuler L.A., Hurley
                                                                                                                                                21
                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PLACENTAL PROLACTIN-RELATED PROTEINS MAY PLAY A SPECIFIC ROLE DURING GESTATION. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                              CLLLLLLMSNLLLC
                                                                                                                                                                     CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                       Q28632;
                                                                                                                                                                                                                                                                                                                                                                              PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad.
                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                               Placenta;
                                                                                                                                                                                                                                                                                                                                                       PS00266;
                                                                                                                                                                                                                                                                                                                                           PS00266; SOMATOTROPIN_1;
PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                           IPR001400; SOMATOTROPIN.
                                   (Rel.
                                                          (Rel.
                                                                                                                                                                                             Conservative
                     (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation updat
protein MG147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA30726.1; -.
AAA30727.1; -.
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sci. U.S.A. 84:5650-5654(1987).
                                                                                                                                                                                                                                                       238 F
215 B
238 B
238 B
201 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a prolactin-related mRNA expressed
                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                              ω
4
                                                                                                                                                                      14
                                                                                                                                                                                                          51.4%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ.Γ.
                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
JOINED.
JOINED.
                                                                                                                                                                                              ۲.
                                                                                                                                                                                                                                                  POTENTIAL.

PLACENTAL PROLACTIN-RELATED PROTEIN
BY SIMILARITY.
BY SIMILARITY.
A -> D (IN REF. 2).
A -> C3609F025BEF808 CRC64;
                                                                                                                                                                                                          Score
Pred.
                                                                                   PRT;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                          36;
No.
                                                                                   375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no rest
                                                                                                                                                                                                                     DΒ
                                                                                   A
                                                                                                                                                                                                                     ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                              5
                                                                                                                                                                                                                     Length 238
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in bovine
                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     its
                                                                                                                                                                                             0;
```

```
밁
                    δÃ
                                                                                                          Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                        Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu p.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(195).
                                                                                                                                 TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                     TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma. NCBI_TaxID-2097; [1]
                                                                                                          SEQUENCE
                                                                                                                        TRANSMEM
                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                  EMBL;

    I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

17
                        ۳
                      CKLLLKLLLKLL
CKALLLLLIPLL
                                                                                                                                                                                                                      MG147;
                                                                                                                                                                                                                                   U39695; AAC71365.1;
                                               Similarity
8; Conser
                                                                                                                  1 protein; 41 41 66 86 161 183 22: 234 25 289 30 338 35
                                                Conservative
                                                                                                            A,
28
                     12
                                                                                                                       41
181
181
223
254
309
358
                                                                                                            43188
                                                                                                                                ; Transmembrane; Com
POTENTIAL.
86 POTENTIAL.
81 POTENTIAL.
23 POTENTIAL.
54 POTENTIAL.
50 POTENTIAL.
                                                           51
66
                                                                                                            MW.
                                             Score 36; DB Pred. No. 80; 1; Mismatches
                                                                                                                       POTENTIAL
                                                                                                            Al4AF07D574E8046 CRC64;
                                                                                                                                                                                                           Complete
                                                                                                                                                                                                                                                                    noved. Usage by and for (See http://www.isb-sib.
                                                       DB
80;
                                                                     1;
                                                ω
                                                                     Length 375
                                                Indels
                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelley J.
                                                                                                                                                                                                                                                                                                                                                                                                                    Merrick J.M.,
                                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                               for commercial ib.ch/announce/
                                                0,
                                                                                                                                                                                                                                                                                                                       collaboration -
                                                                                                                                                                                                                                                                                                                      outstation
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                                                                                                                                                                                                                                               ņ
                                                                                                                                                                                                                                                                                                         on
                                                0;
```

Search completed: June 17, 2002, 12:44:48 Job time: 303 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on
    1121
1131
1154
1154
                                                                                                                                                                                                 and is
                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                          seq
seq
                                                                                                                                                                                               No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.
    protein search, using sw
                                                                                                                                                                                                                                                                                                                         SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammaal:*
7: sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                           length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  length:
                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                    10:
11:
12:
13:
14:
15:
15:
                                                                                                                                                                                                                                                                                                                                                                                                                Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.
   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562222 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       June 17,
                                                                                                                                                                                                                                                                                                                                                                                                        Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKLLLKLLKKLLKC 14
                                                                                                                                    .
                                                                                                                                                                                                                                                                                                         sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                    sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
                                                                                                                                                                                                                                                                                                                sp_organelle:*
                                                                                                                                                                                                                                                                                                                                  sp_mammal:*
                                                                                                                                                                                                                                                                                                                                          sp_invertebrate:*
                                                                                                                                                                                                                                                                     sp_vertebrate:*
                                                                                                                                                                                                                                           sp_bacteriap: *
                                                                                                                                                                                                                                                    sp_rvirus:*
                                                                                                                                                                                                                                                           sp_unclassified:*
                                                                                                                                                                                                                                                                              sp_virus:*
                                                                                                                                                                                                                                                                                      sp_rodent:*
                                                                                                                                                                                                                                                                                              sp_plant:*
                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                           2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0 ,
   988
1022
1880
2481
2513
641
219
                                                                                                                                                                                                                                                                                                                                                                                                        n Match 0%
n Match 100%
y first 45 su
                                                               295
106
169
207
216
314
756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002, 12:44:21; Search time 73.61 Seconds (without alignments) 32.902 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version (c) 1993 - 2000
                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapext 0.5
                                       510
    10
10
13
                           018465
0187853
                                                                     3 Q9PSN4
3 Q9DETO
Q05867
                                                                                                Q9VUG7
Q9Z8R1
                                                                                                                 Q9NKD6
Q9ND11
Q94M45
                                                      Q9N8K2
                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                        summaries
           Q9LPM4
Q9ZT73
                                                              Q9CUES
                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mode]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562222
Q05867 saccharomyc
Q9cue5 mus musculu
Q9n8k2 trypanosoma
Q9f122 arabidopsis
Q18465 hirudo medi
Q9fr53 arabidopsis
Q9pm4 arabidopsis
Q9zt73 arabidopsis
Q9zt73 arabidopsis
                                                                                                        Q9nkd6 drosophila
Q9ndil drosophila
Q94m45 streptococc
Q9vug7 drosophila
                                                                                                                                                     Description
                                                                              Q9z8r1 chlamydia p
Q9psn4 sparus aura
Q9det0 dicentrarch
```

Q9NKD6

σ	6	6	51.	6 51.	5 52.	37 52.9	52.		52.	52.	52.	52.	52.	52.	52.	52.	52.	54.	54.	54.	54.	54.	54.	54.	54.	54.	54.	54.
143	120	74	53	36	846	1252	1030	515	481	398	275	191	161	137	116	96	83	2162	2162	2045	1119	754	518	513	437	437	331	248
4	_		_			<u>ت</u>																		_	11	11	11	11
015412	Q05715	Q94LQ5	Q9BC70	Q9M3S5	Q9AIP5	Q9Y0D0	Q19645	Q9GHC4	045540	Q22902	Q9ZDI6	Q9R9K5	Q9LZ38	Q97MS6	074917	Q9LWS8	Q928W1	Q9WKU5	091940	Q9W444	Q19190	Q9ZQZ2	Q94D22	Q9MV03	Q925U1	Q9CZU4	Ħ	Q9ESC4
015412 homo sapien	ß	oryza sat		Q9m3s5 arabidopsis		Q9y0d0 hydra atten	Q19645 caenorhabdi	Q9ghc4 paris thibe	045540 caenorhabdi	Q22902 caenorhabdi	Q9zdi6 rickettsia		Q91z38 arabidopsis	Q97ms6 clostridium	074917 schizosacch	oryza sat		bovine res	0	Q9w444 drosophila	Q19190 caenorhabdi	arabid		Q9mvO3 pharus lati		Q9czu4 mus musculu	mus	Q9esc4 mus musculu

ALIGNMENTS

```
PRESENTATION OF THE PRESEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region prosophila melanogaster: the Adh region.";
Genetics 153;179-219(1999).
                                                                   SEQUENCE FROM N.A.

STRAIN-Y, AND CN BW SP;

Celniker S.E., Abbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.

Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

HOUSTON K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

Zieran L.L., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNW-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 144.0 KDA PROTEIN (RK GENE PRODUCT).
RK OR BG:DS00180.13 OR CG8930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Y, AND CN BW SP;
MEDLINE-99403001; PubMed-10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9NKD6; Q9VJU3;
                                        (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophilidae;
                                        ç
                                        the
                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the genome of
                                                                                                                                                                                                                                                                                                                                      C.M.,
```

```
Q9NDI1
ID Q
AC Q
DT 0
DT 0
DT 0
DT 0
                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                             Qy
                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RX MEDLINE-2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Charlet S., M., Daylar R.G., Champe M., Doletz S.M., Doletz S., Dahlke C., Davenport L.B., Davies P., RA Gerbard M.R., Dowles M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Bodoko K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Bodoko K., Doletz S., Mayraktaroglu L., Garg N.S., Gelbart W.M., Classer K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris M., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Netchum K.A., Market B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Liux J., Mallar Y., Lin X., Mallar Y., Lin X., Marris J., McLeod M.P., McPherson D.H., Nelson K., Nusskern D.R., Pecleb J.M., Nelson D.H., Nelson K., Nusskern D.R., Pecleb J.M., Nelson D.L., Ra Ra Harris M., Wang X., Marylay B., Murphy L., Many A.H., Wang X., Many A.H., Wang X., Wang Saraman D
                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0003255; rk.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003592; LrR_out.
InterPro; IPR003592; LrR_typ.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
SMART; SM00370; LRR; I.
SMART; SM00370; LRR; TYP; 4.
   Q9NDI1;
01-OCT-2000 (
01-OCT-2000 (
01-DEC-2001 (
GLYCOPROTEIN )
                                                                                                 Q9NDI1
                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 13
                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003408; AAF44846.1; -. EMBL; AE003642; AAF53367.2; -.
                                                                                                                                                                                             14
                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                             CKLLLKLLLKLL 12
                                                                                                                                                                                        CPLLLQLLLQLL
                                                                                                                                                                                                                                                                    Similarity 9; Conser
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
N HORMONE RECEPTOR II.
                                                                                              PRELIMINARY
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                                                                60.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                        144031 MW;
                                                                                                                                                                                                                                                            Score 42; DB Pred. No. 85; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                    B4B9E39F942FA0B3 CRC64;
                                                                                        1360 AA
                                                                                                                                                                                                                                                                            . 85;
                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                               Length 1300;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                        0;
```

```
맑
                    Q
                                                                                                       RESULT
Q94M45
                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 9
                                              Matches
                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2001) to the EMBL; AJ302074; CAC48100.1; Hypothetical protein. SEQUENCE 295 AA; 32657 MW
                                                                                                                                 Obregon V., Garcia P., Garcia E., Lopez R., Garcia J.L.; "Complete nucleotide sequence and analysis of the temperate bacteriophage MM1 genome of Streptococcus pneumoniae."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                Streptococcus pneumoniae bacteriophage MM1 Viruses; dsDNA viruses, no RNA stage; Caud
                                                                                                                                                                                                                                        094M45;
01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 32.7 KDA PROTEIN.
                                                                                                                                                                    SEQUENCE FROM N.A. Obregon V., Garcia P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CANTON S.; TISSUE-WHOLE ANIMAL;
MEDLINE-20359836; PubMed-10899142;
MEDLINE-20359836; PubMed-10899142;
MEDLINE-20359836; PubMed-10899142;
                                                                                                                                                                                                         NCBI_TaxID=120574;
                                                                                                                                                                                                                                                                                                   Q94M45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular Cloning, Genomic Organization, Developmental Regulation, and a Knock-Out Mutant of a Novel Leu-Rich Repeats-Containing G Protein-Coupled Receptor (DLGR-2) from Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 10:924-938(2000)
EMBL; AF142343; AAF66608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eriksen K.K., Hauser F., Grimmelikhuijzen C.J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RK OR BG:DS00180.13 OR CG8930.

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q57815; 1D3Y
                                                                                                                                                                                                                                                                                                                                                          14 CPLLLQLLLQLL
                    1 CKLLLKLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                1 CKLLLKLLKLL 12
                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1360 AA;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pled Recept.
10:924-938(2000).
                                                                                           protein.
32657 MW;
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                    12
                                                                                                                                                                                                                                                                                                                                                           25
                                                      58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               150731 MW;
                                                     . 78;
                                                                                                                                                                                                                RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                           ω,.
                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB
Pred. No. 88;
2; Mismatches
                                                     Pred.
                                                               Score 41;
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                 71A01307E78B6ACF CRC64
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7D435155B4F6F612 CRC64;
                                                     No
                                                  DB
35;
                                                                                                                                                                                                                                                                                               295 AA
                                                                                                                                                                                                                                                                                                                                                                                                             DB
88;
                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                         1;
                                                               Length 295
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1360;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soendergaard
                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                   0;
```

```
RESULTATION OF THE COLOR OF THE
RESULT |
Q9Z8R1
ID Q9Z8
                                                                                                                                                                                                                                                                                                                                                                                                                                  RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., El M.D., Hoskins R.A., Galle R.F., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Barlaw R.H., Doyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Ballawi R.B., Barnadal J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Brossperier G., Perraz C., Ferriera S., Fleischmann W., Folier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., Ra Jalail M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A., Kinmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z., Ra Jakov P., Lei Y., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z., Ra Jakov P., Lei Y., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z., Ra Merison D.R., Nelson K.A., Mixon K., Nusskern D.R., Pacleb J.M., Ra Hariss M., Bullon K., Nixon K., Nusskern D.R., Pacleb J.M., Ra Hariss R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang X., Ferrac R., Venter E., Wang A.H., Wang X., Ra Williams S.M., Woodage T., Wooday M., Strong G., Jaho Q., Jaheng L., Kheng G., Jaho W., Strong G., Zhao Q., Jaheng L., Sheng L., Theng G., Jaho Q., Jaheng L., Sheng L., Sheng L., Perrac J.C., Zhan M., Strong G.
                                                                                                                                                      Вp
                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                     Query Match
Best Local
      Q9Z8R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VUG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG13476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                         77
                                                                                                                                                                                     | 1 CKLLLKLLKLLK
| 1:|||::|:|:|:
                                                           5
                                                                                                                                                                                                                                                                         Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                         Conservative
      PRELIMINARY;
                                                                                                                                                                                                           13
                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                         l; CG13476.
12193 MW;
                                                                                                                                                                                                                                                                                                  57.1%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                     Score
Pred.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      92041B063C951FC4 CRC64,
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                              40;
   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106
                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                 Length 106
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      0
```

```
RRN COX SPARSON COX SCALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLTel. 1
01-DEC-2001 (TrEMBLTel. 15
HYPOTHETICAL 18.2 KD. CPN0277 OP CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Z8R1;
01-MAY-1999
01-MAY-1999
01-DEC-2001
SEQUENCE.
MEDLING-95291367; PubMed-7773329;
                                                                                                                            Sparus aurata (Gilthead sea bream).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Acanthomorpha; Acanthopterygii; Percomor
Sparidae; Sparus.
                                                                                                                                                                                                                                                                      Q9PSN4;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; "Ast. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete SEQUENCE 169 AA; 18203 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shirai M., Hirakawa H., Kimoto M., Tabuchi
Shiba T., Ishii K., Hattori M., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                     SOMATOLACTIN, SL
                                                                                                                                                                                                                                                                                                                                                                       Q9PSN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; CP0481; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVLQVIIKLIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ic Acids Res. 28:2311-2314(2000).
AE0001613; AAD18426.1; -.
AE002208; AAF38311.1; -.
AP002546; BAA98487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR CPJ0277 OR CP0481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10, Created)
10, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                              13,
13,
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome.
4A3B2967C18A7424 CRC64;
                                                                                                                                                            Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 32;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabuchi M., Kishi F., Ouchi K., hara S., Nakazawa T.;
                                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                            Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
rpha; Perciformes; Percoide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MoPn
                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s.,
```

```
RESULT
QDETO
ID QQ
AC QQ
AC QQ
DT QQ
DT QQ
DT QQ
OC QC
               Q05867
ID Q0
AC Q0
DT 01
DT 01
DT 01
DT 01
CH CH
                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RT
RT
DR
DR
DR
DR
DR
DR
DR
DR
DR
Q05867 PRELIMINARY;
Q05867;
Q05867;
Q1-NOV-1996 (TrembLrel. 01, C:
Q1-NOV-1996 (TrembLrel. 01, L:
Q1-JUN-2001 (TrembLrel. 17, L:
CHROMOSOME XII COSMID 8003.
YLR283W OR L8003.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DETO;
Q9DETO;
Q9DETO;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (PRECURSOR (FRAGMENT)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Company R., Calduch-Giner J. "CDNA cloning and sequence somatolactin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dicentrarchus labrax (European sea bass).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Moronidae; Dicentrarchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00836;
                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=13489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DET0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001400; SOMATOTROPIN fam; PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00103; hormone; 1.1.

PRINTS; PR00836; SOMATOTROPIN.

PROSTTE; PS00266; SOMATOTROPIN.1; 1.

PROSITE; PS00338; SOMATOTROPIN.2; 1.

SEQUENCE 207 AA; 23888 MW; FDA8BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Somatolactin, a novel pituitary p
characterization from Sparus aurat
Mol. Mar. Biol. Biotechnol. 4:117-
HSSP; P01241; laxI.
InterPro; IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                      ű
                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ģ
                                                                                                                                                                                                                                           MEILLKLLKC
                                                                                                                                                                                                                                                                                   LKLLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Physiol. 127:183-192(2000).
AJ277390; CAC16116.1; -.
P01241; 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEILLKLLKC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLLLKLLKC
                                                                                                                                                                                                                                                                                                                   Similarity 70.07; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00266; SOMATOTROPIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                       1
<1
10
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calduch-Giner J.A., Mingarro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                     9
216
25010 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                         57.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pituitary protein: isolation Sparus aurata."; hnol. 4:117-122(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
                                     Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                              Score 40; DB Pred. No. 39; 3; Mismatches
                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
SOMATOLACTIN.
; 95CBB324A6069F00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB Pred. No. 38; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDA8BBBEC9737271 CRC64;
                                                                                                                              314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
rpha; Perciformes; Percoidei;
                                                                                                                              ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M., Perez-Sanchez J.;
ea bass (Dicentrarchus
                                                                                                                                                                                                                                                                                                                                                           13;
                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                        Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 207;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         labrax)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

ŝ

```
Query Match
Best Local s
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. SEQUENCE FROM N.A.

MEDLINE=97313267; PubMed=9169871;
A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge Johnston M., Hillier L., Riles L., Dubois E., Dusterhoft A., Andre B., Ansorge A. Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., A. Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., A. Heuss-Neitzel D., Hilbert H., Hilder F., Kleine K., Kotter P., A. Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D., A. Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D., A. Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose A. Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., White M., Weiler M., 
      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alazwa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Blake J., Roffelli D., Rodinga N., Caratari D., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9CUE5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
4931427F14EK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CUE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4931427F14RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1997) to the EMBL; U17243; AAB67328.1; SGD; S0004273; YLR283W. SEQUENCE 314 AA; 36574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cherry J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pauley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The nucleotide sequence of Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CKLLLKLLLKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKITTALLLQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
   Boffelli D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOV-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
Bojunga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the !
1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB
Pred. No. 54;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2CEFDB5C73D57B08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome XII.";
                                                                                                                                                                         Ishii Y.,
Fukuda S.,
manaka I.,
Saito R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pohl T.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ansorge W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wedler E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

В Qy

```
RESULT
Q9FL22
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
OC SP
OC EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARESULT PAR
                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       뫄
                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hall N., Bowman S., Quail M., Ivens A.C., Kay M.
Lennard N.J., Clark L.N., Harris B.R., Melville of Gerrard C., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ da:
EMBL; AL359782; CAB95541.1; -
Interpro: IPR000847; HTH_LYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY; UNKNOWN_1.
HYPOTHETICAL PROTECH.
SEQUENCE 988 AA; 107318 MW; EFB3A38C56AE6E85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9N8K2;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                     Q9FL22;
Q9FL22;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
QENOMIC DNA, CHROMOSOME 5, P1 CLONE:MPL12.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-TREU927; Hall N., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma brucei.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK016477; BAB30259.1; -.
MGD; MGI:1921612; 4931427F14Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
"Functional annotation of a
                                                                                                                                                                                                                                     Q9FL22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHR1.297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9N8K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001)
EMBL; AK016477; BAB30259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wynshaw-Boris A., Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                  432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                2 KLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KLLLKLLKLLKC
osids II; Brassicales;
[_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                  ELHLKLVLRLLQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLTLPLIGKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 69.3
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    756
756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756
86030 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
                                                                                                                                                                                                                                                                                                                                                  444
                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ang K.H., Weitz C., Whittaker C., Wilming K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 11;
Pred. No. 1.1e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.40
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19A6BE7FD7853652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFB3A38C56AE6E85
                                                                                                                                                                                                                                   1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bray-Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                             Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
```

```
RESULT
018465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physically assigned Pl and TAC o
DNA Res. 5:131-145(1998).
EMBL; AB010698; BAB11095.1; -.
InterPro; IPR003107; HAT.
SMART; SM00386; HAT; 4.
SEQUENCE 1022 AA; 117365 MW;
                  Pfam; PF00041; fn3; 4.
Pfam; PF00047; ig; 6.
PRINTS; PR00014; FNTYPEI
SMART; SM00060; FN3; 4.
SMART; SM00408; IGC2; 4.
SMART; SM00410; IG_like;
                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                    018465;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-92198663; PubMed-1550678;

Johansen K.M., Kopp D.M., Jellies J., Johansen J.;

"Tract formation and axon fasciculation of molecularly distinct peripheral neuron subpopulations during leech embryogenesis.";
                                                                                                                                                                                                                                                                                                                              Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hir
Arynchobdellida; Hirudiniformes; Hirudinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Kotani
Tabata S.;
                                                                                                                                         J. Cell Biol. 138:143-157(1997).
EMBL; U92813; AAC47654.1; -.
HSSP; P20241; ICFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana features of the regions of 1,381,565 bp cover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM
                                                                                                                      InterPro;
                                                                                                                                                                                    superfamily
                                                                                                                                                                                            Huang Y., Jellies J., Johansen "Differential glycosylation of
                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-97362067;
                                                                                                                                                                                                                                                Neuron
                                                                                                                                                                                                                                                                                                                                                              TRACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98344145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
                                                                                 InterPro;
                                                                                          InterPro;
                                                                                                  InterPro;
                                                                                                              InterPro;
                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6421;
                                                                                                                                                                         formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477
                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CKLLLKLLLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKLLLEELMRLL
                                                                                                                                                                                                                                              8:559-572(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conser
                                                                                                             IPR000087;
IPR003962;
IPR003961;
                                                                                        IPR003598;
IPR003600;
                                                                               IPR003006;
                                                                                                                                                                                                                                                                                                                                                                      3 (TrEMBLrel. 05,
3 (TrEMBLrel. 05,
1 (TrEMBLrel. 19,
                                                                                                                                                                                    members,
 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
           domain;
                    IGc2; 4.
IG_like; 2.
                                                  FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9679202;
                                                                                                                                                                                                                PubMed=9214388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                             FnIII_re,
FN_III.
Ig_c2.
Ig_like.
Ig_MHC.
n; Repeat.
199865 MW
                                                                                                                                 Collagen.
                                                                                                                                                                                 ylation of tractin and Leecht regulates neurite extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%;
66.7%;
                                                                                                                      _repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB Pred. No. 1.5e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW.
                                                                                                                                                                                                                                                                                                                                                                                            Created)
 174EC84DAC540DF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B59AC43225E4A17F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; DB 10;
No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato
                                                                                                                                                                                             ohansen J.;
and LeechCAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         covered
                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                Hirudinida;
dae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γģ
                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1022;
 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         twenty one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [H]
                                                                                                                                                                                     fascicle
                                                                                                                                                                                             two novel
                                                                                                                                                                                                                                                                                                                                           Hirudinea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                             Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

Query Match Best Local S Matches

Similarity 9; Conser

Conservative

57.1%;

Score 40; DB 5; Li Pred. No. 2.4e+02; l; Mismatches 4;

Length 1880;

Indels

0;

Gaps

0;

ΔÃ

14

```
RESULT
Q9ER53
ID Q9ER53
ID Q9
AC Q9
DT Q1
DT Q1
DT Q1
OC Q9
OC E P
OC E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
STRAIN-CY. COLUMBIA,
STRAIN-CY. COLUMBIA,
Sakano H., Liu S.X., Yu G., Lee J., Lenz C., Pham P., Torit
Sakano H., Liu S.X., Yu G., Lee J., Lenz C., Pham P., Torit
Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B.
Chin C., Chiou J., Eroks S., Bueler E., Chao Q., Co
Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim
Miranda M., Nguyen M., Palm C., Shinn P., Southwick A., Da
Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC F2J10 from Arabidopsis thaliana chron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IFR003151; FAT.
InterPro; IFR003152; FATC.
InterPro; IFR003152; FATC.
InterPro; IFR000403; FT3_PT4_kinase.
Pfam; PF02259; FAT; 1.
Pfam; PF02250; FATC; 1.
Pfam; PF02260; FATC; 1.
Pfam; PF00454; PT3_PT4_kinase; 1.
SMART; SM00146; PT3_PT4_kinase; 1.
SMART; SM00146; PT3_FT4_KINASE_1; 1.
PROSITE; PS50290; PT3_4_KINASE_3; I.
SEQUENCE 2481 AA; 279187 MW; DA663;
                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LPM4;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    F2J10.9
                                                                                                                                                                                                                                                                                                                                                                                                       F2J10.9 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LPM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Menand B., Nussaume I., Meyer C.,
"Mutation in AtTOR affects embryo
Submitted (AUG-1999) to the EMBL/G
EMBL; AF178967; AAG43423.1; -.
HSSP; P42345; IFAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          785 LLLGLLLKLLK 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9FR53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FR53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LLLKLLLKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKLLLLLLLLLLC :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1771
                                                                                                                                                                                                                                                                                                                                                                                                                      15,
15,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16,
16,
                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DA663EA9A9366F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnos T., Bouchez development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                          chromosome 1. ";
                                                                                                                                                           Toriumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracheophyta;
                                                                                                           Conn L.,
                                                                     Davis
                                                                                                                                        В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robaglia
                                                                Lam B., R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                              Liu A.,
                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ი
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

:

Search cor Job time:

completed: me: 298 sec

June

17,

2002, 12:44:23

```
ACCOMPANDATION ACCOMP
                     В
                                                              Qy
                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q9ZT73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO0315; FAT.
InterPro; IPRO0315; FATC.
InterPro; IPRO03403; PI3_PI4_kinase.
Pfam; PF02259; FAT; 1.
Pfam; PF02250; FATC; 1.
Pfam; PF00454; PI3_PI4_kinase; 1.
SMART; SM00146; PI3_FI4_kinase; 1.
PROSITE; PS00915; PI3_4_KINASE_2; 1.
PROSITE; PS00916; PI3_4_KINASE_2; 1.
PROSITE; PS00916; PI3_4_KINASE_2; 1.
PROSITE; PS00916; PI3_4_KINASE_3; 1.
SEQUENCE 2513 AA; 282911 MW; A4I
                                                                                                                                                                                                           PROSITE; PS50297; ANK_REP_REGION;
ANK repeat; Hypothetical protein;
SEQUENCE 641 AA; 70466 MW; ECI
                                                                                                                                                                                                                                                                              InterPro; IPR002110; ANK. Pfam; PF00023; ank; 9. SMART; SM00248; ANK; 2.
                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF071527; AAD11587.1; -.
EMBL; AL161496; CAB7833.1; -.
                     304
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. COLUMBIA;
Huang E.N., Parnell L.D., de la E
Dedhia N.N., McCombie W.R.;
"Genomic sequence of Arabidopsis
18.8 cM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopsisermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TIEMBLIEL 10, CI
01-MAY-1999 (TIEMBLIEL 10, La
01-DEC-2001 (TIEMBLIEL 19, La
HYPOTHETICAL 70.5 KDA PROTEIN.
P9H3.7 OR AT4603450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZT73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2000) to the EMBL; AC015445; AAF76442.1; HSSP: P42345; 1FAP.
                                                      5 LKLLLKLLKC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797 LLLGLLLKLLK
VKIFLKLLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLLKLLLKLLK 13
                                                                                                      Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 90.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FEB-1999)
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
              313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807
                                                                                                                            55
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FATC.
PI3_PI4_kinase.
                                                                                                                         .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the EMBL/GenBank/DDBJ
                                                                                          Score 39; DB
Pred. No. 1.4e
2; Mismatches
                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                      N; 1.
in; Repeat.
ECD57973640403CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bastide M., Schutz K., Habermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thaliana BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A4B9740321AC5261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
No.
                                                                                        DB 10;
1.4e+02;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F9H3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                     Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2513;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tracheophyta;
udicots; Rosidae;
                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

THIS PAGE BLANK (USPTO)

Run

```
Minimum
Maximum
                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                 ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
   score greater t
and is derived
                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB DB
                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq
 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: //gn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: //gn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                                                                                                                                                                                            is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
  BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-367-714A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKLLLKLLKLLKC
                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002, 12:42:05; Search time 34.71 Seconds (without alignments) 9.852 Million cell updates/sec
  GenCore version (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapext 0.5
       US-09-000-692-1
US-08-569-188-8
PCT-US94-07019-1
US-08-569-188-1
US-08-569-188-1
US-08-569-188-1
US-08-569-188-1
PCT-US94-07019-1
PCT-US94-07019-1
PCT-US94-07019-1
PCT-US94-07019-1
US-08-569-188-3
US-08-818-252-3
US-08-818-252-3
US-08-818-252-3
US-08-818-253-3
US-08-818-252-3
US-08-818-253-3
US-08-569-188-5
PCT-US91-05047-60
PCT-US91-05047-61
US-07-725-331-62
PCT-US91-05047-63
US-07-725-331-63
PCT-US91-05047-63
US-07-725-331-63
PCT-US91-05047-63
                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231628
                sequence 10, Appl
sequence 11, Appl
sequence 12, Appl
sequence 11, Appl
sequence 11, Appl
sequence 11, Appl
sequence 13, Appl
sequence 3, Appl
sequence 3, Appl
sequence 3, Appl
sequence 5, Appl
sequence 60, Appl
sequence 60, Appl
sequence 61, Appl
sequence 61, Appl
sequence 61, Appl
sequence 62, Appl
sequence 62, Appl
sequence 63, Appl
sequence 61, Appl
sequence 62, Appl
sequence 62, Appl
                                                                                                                                                                                                                                                                Description
sequence
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                            Sequence
5, 1
60,
60,
19,
61,
61,
62,
63,
63,
                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                 Appli
Appli
Appli
Appli
                                                                                                                                밁
                                                                                                                                                ρy
                                                                                                                                                                                                                  US-09-000-692-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-000-692-1
                                                                                                                                                                   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                   FEATURE:
```

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	38
52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	54.3
18	18	18	18	18	18	18	17	17	17	17	16	16	16	16	14	14	21
ហ	u	4	4	4	N	Ν	Ģ	G	ν	ν	σ	5	2	N	ر.	М	Н
PÇT-US94-07019-15	PCT-US94-07019-6	us-09-296-089-36	US-08-958-993A-12	US-08-960-054A-12	US-08-569-188-15	US-08-569-188-6	PCT-US94-07019-14	PCT-US94-07019-4	US-08-569-188-14	US-08-569-188-4	PCT-US94-07019-13	PCT-US94-07019-2	US-08-569-188-13	US-08-569-188-2	PCT-US91-05047-1	US-07-725-331-1	US-08-944-133-13
15,	Sequence 6, Appli	Sequence 36, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 15, Appl	Sequence 6, Appli	Sequence 14, Appl	Sequence 4, Appli	•	Sequence 4, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 13, Appl

ALIGNMENTS

```
RESULT 2
US-08-569-188-8
; Sequence 8, Application US/08569188
; Sequence 8, Application US/08569188
; Patent NO. 5847047
; GENERAL INFORMATION:
APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
; MUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/000,692
CURRENT FILING DATE: 1997-12-30
EARLIER APPLICATION NUMBER: 08/778657
EARLIER FILING DATE: 1997-01-03
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application Patent No. 6339067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SLATTUM, PAUL M
APPLICANT: HANSON, LISA J
TITLE OF INVENTION: A PROCESS OF MAKING A COMPOUND
TITLE OF INVENTION: FROM A TEMPLATE DRUG
FILE REFERENCE: TPCIP000692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WOLFF, JON A
APPLICANT: HAGSTROW, JAMES E
APPLICANT: BUDKER, VLADIMIR G
APPLICANT: TRUBETSKOY, VLADIMIR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Unknown Organism: AMPHIPATHIC
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                 1 CKLLKKLLKLWKKLLKKLKC
                                                                                                                                                                                                                                                                                                                  1 CKLLLKL-----LLKLLKC
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                        64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09000692
                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         45;
No.
                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY FORMING
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A POLYMER
                                                                                                                                                                                                                                                                                                                                                                          6;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

۲,

COUNTRY: 19898

```
TITLE OF INVENTION: NOVEL ANTIMICROBIAL NUMBER OF INVENTION: COMPOSITIONS COMPUTER SEQUENCES: 15 SEQUENCES: 16 SEQUENCES: 17 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLING DATE:
PILASSIFICATION: 525
APPLICATION UNBER N.
ATTORNEY DATE:
WAME: LIND ANAMETHY FOR APPLICATION WHERE 2, 1993
AFTILING TON WHERE 2, 1993
ATTORNEY DATE:
WAME: LIND ANAMETHY FOYD
REGISTRATION ANAMETHY FOYD
REFERENCE, DOCKET NUMBER: CF-929;
TELEPANICATION INFORMATION: 302-773-8112
SEQUENCE OF SEQUENCE CHARACTED IN NO:
LENGTH: 14 AMINOTION: 8:
TYPE: AMINO ACID
TOPOLOGY: ESS UNKNOWN
WOLDCHE TYPE: WINNOWN
WOLDCHE TYPE: WINNOWN
US-08-569-188-8: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 8, Application PC/TUS9407019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 14;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:

MEDIUM TYPE:
COMPUTER: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
ADDITOR MINDERD. TO MARKEN MINDOWS 95
ADDITOR MINDERD. TO MARKEN MINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                              57.1%; Score 40; DB 5; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y: DELAWARE
TGROEN STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR-9295-A
                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 (7.0)
                                                                                                                                                                            0;
                                                                                                                                                        _{\rm Gaps}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                 ,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _{
m Gaps}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,0
                                                                                                                                                                                                           RESULT 5
US-08-569-188-10
Sequence 10, Application US/08569188
Fatent No. 5847047
GENERAL INFORMATION:
SHARON LPRETTA HAYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICASSIFICATION: 525
APPLICATION DATA:
APPLICATION UMBER: 08/082.8
APPLICATION UMBER: 08/082.85
APPLICATION UMBER: 0993.85
APPLICATION UMBER: 0993.85
APPLICATION AND APPLICATION:
APPLICATION AND APPLICATION:
APPLICATION UNDER: 33.692
TELEPANTION UNDER: 33.692
TELEPANTION UNDER: 33.692
TELEPANTION FOR SET NUMBER: CR-92:
INFORMATION: 302-773-0164
LENGTH: 16 ANTIONALIS: 1:
SEQUENCE CHARACTERISTICS: 1:
TYPE: annino acids
TORNANDESS: unknown
US-08-569-188-I TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                APPLICANT:

TITLE OF INVENTION. LPRETTA HAYNIE
NUMBER OF ENCHANCES: NOVEL ANTIMICORBIAL COMPOSITIONS
ADDRESSOME ADDRESS: 18
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
                                 COUNTRY: UN
ZIP. 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KLLLKLLLKLLK
| |||| ||| |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3 tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHARON: LPRETTA HAYNIE
TITLE OF INVENTION: LOVEL ANTIMICORBIAL COMPOSITIONS
CORRESPONDENCES: 18
ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPOSITIONS
STREET: 1007 MARKET STREET
WILMINGTON
STATE: DELAWARE
INTTED STATES DE LAWARE
INTTED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
US-08-569-188-1
Sequence 1, Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER TOWN
MEDIUM TYPE; DISKETTE, 3.50 INCH
COMPUTER; IBM PC COMPATIBLE
CURRATING SYSTEM; MICHOSOFT WINDOWS 95
THE APPLICATION DATA; TOWN WINDOWS 95
THE APPLICATION DATA; TOWN AT AR APPLICATION DATA; TOWN AT APPLICATION DATA; T
UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08569188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKLLKLLKKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KLLLKLLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.18;
83.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/082,852
22, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.3; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,0
```

В

2 KKLLKLLKKLLK 13

-US94-07019-8

ACTERISTICS:
APE: Amino anino acids
STRANDEDNESS: unknown
PCT-US94-07019-8

Quer-

Ouery Match Best Local Similarity 57.1 Matches 10: Conservative

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: ur ; MOLECULE TYPE: US-08-569-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-569-188-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08569188 Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,85:
FILING DATE: JUNE 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 302-773-0164 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/0
FILING DATE: JUNE 22, 19
ATTORNEY/AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: LINDA AXAMETHY FLOYD REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9295-A TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 10; Conserv
                                                                                                                                                                                                                                                MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/569,188 FILING DATE:
                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                                              19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                       E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B: DISKETTE, 3.50 INCH
IBM PC COMPATIBLE
SYSTEM: MICROSOFT WINDOWS 95
MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                                                                                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
83.3%;
                                                                                                                     08/082,852
2, 1993
                                                                                                                                                                                                               US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1993
                                           CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
```

```
; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-569-188-11
 밁
                             Qy
                                                                                                                                            ; MOLECULE TYPE: US-08-569-188-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-569-188-12
                                                              Matches
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08569188 Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/082,85
FILING DATE: JUNE 22, 1993
ATTORNEY_AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE_POCKET NUMBER: CR-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     TELEFAX: 302-773-0164 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: MOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1007 MAR CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
2 KILLKILLKILK 13
| ||||| ||||
4 KKILKILKKILK 15
                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KLLLKLLKLLK 13
| ||||| ||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KKLLKLLKKLLK 15
                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                                       302-892-8112
302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNITED STATES OF AMERICA
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                            57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                               08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.50 INCH
                                                                                                                                                                                                                                                                                                                   CR-9295-A
                                                                 0,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                            Score 40; DB
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2:
                                                                                             Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
```

RESULT 8 PCT-US94-07019-1

0

Sequence 1, Application PC/TUS9407019 GENERAL INFORMATION:

```
Query Match
Best Local Similarity
Thes 10; Conserve
                                                                                                                                        TOPOLOGY: unknown

MOLECULE TYPE: peptide
PCT-US94-07019-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
PCT-US94-07019-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δδ
                                                                                                                                                                            CURRENT APPLICATION DATA;

APPLICATION NUMBER: PCT/US94

PRIOR APPLICATION DATA;

APPLICATION DATA;

APPLICATION DATA;

APPLICATION UMBER: 08/082,8

FILING DATE: JUNE 22, 193

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: Inknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOLECULE TYPE: PCT-US94-07019-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/082,8
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
GMDANTANERONEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: MACINTOSH 6.0
OPERATING SYSTEM: MACINTOSH 6.0
SOSTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/070
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL A TITLE OF INVENTION: COMPOSI NUMBER OF SEQUENCES: 15 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                               COMPUTER: MACINTOSH 6.0 OPERATING SYSTEM: MACINTOSH 6.0 SOFTWARE: MICROSOFT WORD, 4.0
4 KKLLKLLKKLLK 15
                             2 KLLLKLLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KLLLKLLKLLK 13
| ||||| ||||
4 KKLLKLLKKLLK 15
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                        57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                COMPOSITIONS
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL ANTIMICROBIAL
                                                                                                                                                                                                                                                                                                     PCT/US94/07019
                                                                                                                                                                                                                                                                         08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US94/07019
                                                   0;
                                                                     Score 40; DB
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 5;
Pred. No. 4.3;
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                  DB 5;
                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16;
                                                   Indels
                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

RESULT

10

밁

4 KKLLKLLKKLLK 15

Дb Qy

```
QΥ
                                                                                                 PCT-US94-07019-12
                                                                                                                             APPLICATION NUMBER: 08/082,8:
APPLICATION NUMBER: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
PCT-US94-07019-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                Matches
                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US94-07019-11
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Applicat: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-07019-11 : Sequence 11, Application PC/TUS9407019 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6.0
SOSTWARE: MICROSOST WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/0701:
PRIOR APPLICATION DATA:
OR/OR2.852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                 APPLICATION NUMBER: 1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           OPERATING SYSTEM: MACINTOSH 6.0 SOFTWARE: MICROSOFT WORD, 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: unk
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                         Local Similarity 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
2 KLLLKLLKLLK 13
                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                             Application PC/TUS9407019
                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                     MACINTOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                       57.1%;
                                                                                                                                                                                                                                                                                                                                                           NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                      08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVEL ANTIMICROBIAL COMPOSITIONS
                                                                                                                                                                                                                                                  PCT/US94/07019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT/US94/07019
                         0; Mismatches
                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 5;
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                      DB 5;
                                                Length 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                 0;
```

0;

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-569-188-3
                                                                                                                                                                                                                                                                                                        US-08-818-253-39
                                                                                                                                                                                                                                                     Patent No. 5998204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Sequence 39, Application US/08818253
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08569188
Patent No. 5847047
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULT 12 -
-08-569-188-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: LINDA AXAMETHY FLOYD REGISTRATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: CR-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: JUNE 22,
                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100,
CITY: WILMINGTON
CTIAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
                                                   COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
 COMPUTER:
                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                            5 KKLLKLLKKLLK 16
                                                                                                                                                                                                                                                                                                                                                                                                           2 KLLLKLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19898
                                                                                                  La Jolla
                                                                                   CA
                                                                                                                  4225 Executive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%;
83.3%;
                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
•••
                                                                                                                 Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

0;

COMPOSITIONS 15

```
밁
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Calmodulin binding peptide-2 US-08-818-252-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                   QΥ
                                                                                                                                                                                                     Query Match
Best Local Similarity
Whiches 10; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: US-08-818-253-39
                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-818-252-39
                                                                                            PCT-US94-07019-3
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                           Sequence 3, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6197928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TSIEN, ROGER Y.
APPLICANT: MIYAWAKI, ATSUSHI
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
FILE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT EPPLICATION UMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 619/678-507
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 072
TELECOMMUNICATION INFORMATION: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-MAR-1997 PRIOR APPLICATION DATA:
                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                        4
                                                                                                                                                                      2 KLLLKLLLKLLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KLLLKLLLKLLK 13
                                                                                                                                                        KKLLKLLKKLLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08818252B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 amino acids
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: Windows 95
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                    57.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%;
83.3%;
                              NOVEL ANTIMICROBIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/818,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07257/043001
                                                                                                                                                                                                                  Score 40; DB Pred. No. 4.6; O; Mismatches
                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

COMPUTER READABLE FORM:

WEDIUM TYPE: ETLOPPY DISK
COMPUTER: MACINTOSH 6.0
COMPUTER: MACINTOSH 6.0
SOFTMARE: MICROSOFT WORD, 4.0
SOFTMARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION NUMBER: PCT/US94/07019
APPLICATION NUMBER: PCT/US94/07019
PATOR APPLICATION NUMBER: PCT/US94/07019
APPLICATION NUMBER: PCT/US94/07019
APPLICATION NUMBER: PCT/US94/07019
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
STRANNEDRESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
ANACECULE TYPE: peptide
PCT-US94-07019-3

QUETY MATCH
Best Local Similarity 83.3%; Pred. No. 4.6;
MATCHES 10; Conservative 0; Mismatches 2; Indels 0; Gaps
QUETY MATCH
MATCHES 10; CONSERVATIVE 0; Mismatches 2; Indels 0; Gaps
O;
Search completed: June 17, 2002, 12:42:05